STIC-Biotech/ChemLib

F	rom
•	

Sent:

Slobodyansky, Elizabeth Tuesday, December 31, 2002 12:39 PM STIC-Biotech/ChemLib

To: Subject:

09/873,075

Please search for case 09/873,075:

SEQ ID NO: 1 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652 CM1 10D11 703-306-3222

mail box 10D01

Point of Contact: Mona Smith Technical Information Specialist CM1 6A01 Tel: 308-3278

Searcher: H. Sm. Toll	
Phone:	
Location:	_
Date Picked Up: 1/2/3	
Date Completed: 1 3 5	
Searcher Prep/Review: 5	
Clerical:	
Online time: 4	

TYPE OF SEARCH:
NA Sequences:
AA Sequences:/
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (whe	ere applic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):	

THIS PAGE BLANK (USPTO)

```
January 2, 2003, 15:04:44; Search time 15 Seconds (without alignments) 380.536 Million cell updates/sec
                                                                                                                                                                                                                US-09-873-075A-1
999
1 QLGAIENGLESGSANACPDA......SYTIEARGEAARFLRDRIRA 194
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                         262574 segs, 29422922 residues
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                  Run on:
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgg2_6/ptodata/1/laa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:* Issued_Patents_AA:' Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2, Appli	ς,	Sequence 8, Appli	9	197,	Sequence 197, App	Sequence 154, App	154,	154,	154,	154,	112,	112,	112,	Sequence 112, App	112,	3, Ar	ω	2, 1	50,	8,	18	7, 1	w	Patent No. 5196511	Seguence 6, Appli	9
SUMMARIES	ID	US-08-817-997A-2	US-09-177-234-3	US-09-177-234-8	US-09-177-234-6	US-09-095-855-197	US-09-205-426-197	US-08-997-080-154	US-08-997-362-154	US-09-095-855-154	US-09-324-542-154	US-09-205-426-154	US-08-997-080-112	US-08-997-362-112	US-09-095-855-112	US-09-324-542-112	US-09-205-426-112	US-08-817-997A-3	US-08-804-227C-8	US-08-804-198-2	US-08-282-197C-50	US-08-217-327-8	US-09-355-166-18	US-09-409-648-7	US-09-409-648-8	5196511-2	US-09-647-540A-6	US-08-657-641-6
	DB	7	4	4	4	4	4	N	~	4	7	4	~	~	4	4	7	~	~	7	ď	-	4	4	4	9	4	7
	Query Match Length DB	229	231	232	232	285	285	748	748	748	748	748	167	167	167	167	167	28	4550	4550	345	592	200	1039	1039	1039	414	428
dР	Query Match	100.0	50.1	50.0	48.2	14.5	14.5	11.9	11.9	11.9	11.9	11.9	11.6	11.6	11.6	11.6	11.6	11.5	0.6	9.0	8.9	8.9	8.7	7.7	7.7	7.7	7.6	9.7
	Score	666	500.5	499.5	482	145	145	119	119	119	119	119	116	116	116	116	116	114.5	06	06	83	88	86.5	76.5	76.5	76.5	9.6	9.2
	Result No.	П	7	3	4	Ŋ	9	7	œ	O	10	11	12	13	14	15	16	17	18	19	20	21	22	. 23	24	25	56	27

Sequence 6, Applia Sequence 6, Applia Sequence 7, Applia Sequence 1, Applia Sequence 22, Applia Sequence 26, Applia Sequence 26, Applia Sequence 26, Applia Sequence 16, Applia Sequence 4, Applia Sequence 4, Applia Sequence 4, Applia Sequence 2, Applia Sequence 3, Applia Sequence 4, Applia Sequence 5, Applia Seq
PCT-US94-07233-6 US-08-707-793A-6 US-08-8-707-792A-6 US-08-8-708-792A-6 US-08-308-872B-7 US-08-308-872B-6 US-08-392-459-22 US-08-392-459-22 US-08-392-459-22 US-08-392-459-22 PCT-US91-0825-22 PCT-US91-0825-22 PCT-US91-0825-22 PCT-US91-084-8 PCT-US93-04384-8 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-16 PCT-US93-04384-18 US-09-509-814A-1
0147445000000044
224 2224 2224 10564 11451 11453 11454 11454 11454 11454 11454 11454 11454 11454
777777777779 99948 10094
76 75.5 73.5 73 73 73 73 72 73 72 73
20000000000000000000000000000000000000

ALIGNMENTS

```
ö
                                                                         APPLICANT: Sandal, Thomas
APPLICANT: Rauppinen, Sakari
APPLICANT: Rauppinen, Sakari
APPLICANT: Kofod, Lene V.

TITLE OF INVENTION: An Enzyme With Lipolytic
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 58277190 No. 5827719disk Of No. 5827719th America, Inc.
STREET: A05 Lexington Avenue - 64th F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 999; DB 2; L
Best Local Similarity 100.0%; Pred. No. 9.7e-107;
Matches 194; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,997A
CLASSIFICATION: 7435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4316.204
                Sequence 2, Application US/08817997A Patent No. 5827719 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 7435
ATTORNEY/AGENT INFORMATION:
NAME: LAMBILIS, Elias
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4316
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-878-9652
TELEPAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: 229 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                   10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-817-997A-2
JS-08-817-997A-2
                                                                                                                                                                                                                                                                                                       STATE: N
COUNTRY:
```

1 OLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 60

ò

```
SEQ ID NO 8
LENGIH: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-09-177-234-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                      61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                          96 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 155
                                                                                                                121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 KEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAV 122
36 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 IENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                    Sequence 3, 4pplication US/0917234A
Patent No. 6350604
GENERAL INFORMATION:
APPLICANT: Hitayama, Satoshi
APPLICANT: Taira, Rikako
APPLICANT: Borch, Kim
APPLICANT: Borch, Kim
APPLICANT: Gorch, Kim
APPLICANT: Gorch, Kim
APPLICANT: Gorch, Kim
APPLICANT: Gorch, Kim
APPLICANT: Halkier, Torben
APPLICANT: Gorcholl, Karen M.
APPLICANT: Oxenboll, Karen M.
APPLICANT: Halkier, 100ben
APPLICANT: Homes
APPLICATION NUMBER: 501/96
EARLIER APPLICATION NUMBER: 501/96
EARLIER APPLICATION NUMBER: 501/96
EARLIER APPLICATION NUMBER: 501/96
EARLIER PILING DATE: 1996-04-25
EARLIER PILING DATE: 1997-04-22
NUMBER OF SEO ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.1%; Score 500.5; DB 4 50.0%; Pred. No. 1.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 50.0%; Pred. No. 1.8e-
Matches 95; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-177-234-8
; Sequence 8, Application US/09177234A
; Patent No. 6350604
                                                                                                                                                                                                                  ORGANISM: Gliocladium sp.
                                                                                                                                                                                            181 RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
US-09-177-234-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||:|| :|
221 PAAQFLASKI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
                                                                          g
                                                                                                                ò
                                                                                                                                                  g
                                                                                                                                                                                                                            g
                                      ò
                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

```
DAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 IENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 KEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 232;
APPLICANT: Hirayama, Satoshi
APPLICANT: Taira, Rikako
APPLICANT: Taira, Rikako
APPLICANT: Borch, Kim
APPLICANT: Borch, Kim
APPLICANT: Bandal, Thomas
APPLICANT: Halkier, Torben
APPLICANT: Helsen, Torben
APPLICANT: Helsen, Torben
TITLE OF INVENTION: Alkaline Lipolytic Enzyme
FILE REFERENCE: 4698.204-US
CURRENT APPLICATION NUMBER: 500/96
EARLIER APPLICATION NUMBER: 501/96
EARLIER PILING DATE: 1996-04-25
EARLIER FILING DATE: 1996-04-25
SARILER FILING DATE: 1997-04-22
NUMBER: PSCI ID NOS: 8
SOFTWARE: FASTESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 499.5; DB 4
50.5%; Pred. No. 2.3e-49;
live 32; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRNERAL INFORMATION:
APPLICANT: Hirayama, Satoshi
APPLICANT: Taira, Rikako
APPLICANT: Borch, Kim
APPLICANT: Borch, Kim
APPLICANT: Borch, Thomas
APPLICANT: Gandal, Thomas
APPLICANT: Gandal, Thomas
APPLICANT: Melsen, Bjarne R.
TITLE OF INVENTION: Alkaline Lipolytic Enzyme
FILE REFERENCE: 4698.204 US
CURRENT APPLICATION NUMBER: 500/96
EARLIER FILING DATE: 1996-10-22
EARLIER FILING DATE: 1996-04-25
EARLIER FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09177234A Patent No. 6350604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Trichophaea saccata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 50.5
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
US-09-177-234-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 PAAOFLASKI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 EAARFLRDRI 192
```

3

14;

```
68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                               68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 -----SELSGAVKEQVKGVALFGY-TQNLQNRGGIPNYP---RERTKVFCNVGDAVC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SELSGAVKEQVKGVALFGY-TQNLQNRGGIPNYP---RERTKVFCNVGDAVC 163
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                               27 IPTASADPCPDIEVIFARGTGAEPG-LG-WYGDAFVNALRPKVGE---QSVG----TYA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 LESGSANACPDAILIFARGS-TEPCNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                 9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 197, Application US/09205426
Sequence 197, Application US/09205426
Sequence 197, Application US/09205426
Sequence 197, Application US/09205426
Sequence 197, Application Sequence 197
TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Light Office 1000.10024
CURRENT FILING DATE: 1998-12-04
SEARLER APPLICATION NUMBER: 09/095,855
SEARLER FILING DATE: 1998-06-11
EARLIER PLICATION NUMBER: 08/997,362
SEARLER PLICATION NUMBER: 08/997,362
SEARLER PLICATION NUMBER: 08/997,362
SEARLER FILING DATE: 1997-06-12
SEARLER PLICATION NUMBER: 08/997,363
SEARLER PLICATION NUMBER: 08/997,363
SOFTHARE: PLICATION NUMBER: 08/9705,347
SEARLER PLICATION NUMBER: 08/705,347
                                                                                                                                                                                                                                         Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 145; DB 4;
28.6%; Pred. No. 1.6e-08;
tive 31; Mismatches 71;
                                                                                                                                                                                                                                      14.5%; Score 145; DB 4;
illarity 28.6%; Pred. No. 1.6e-08;
Conservative 31; Mismatches 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 TGTLIITPAHLSYT----IEARGEAARFLR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                        INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                          single
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 60; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 60; Conserva
                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                          US-09-095-855-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-205-426-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   음
                                                                                                                                                                                                                                                                                        Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 YTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGEAARFLRDRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 GTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                                                                               16 ACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALAINFLPR 73
                                                                                                                                                                                                                                    Length 232;
                                                                                                                                                                                                                                                                                   56; Indels
                                                                                                                                                                                                                                  48.2%; Score 482; DB 4;
49.7%; Pred. No. 2.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                   33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/095,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 197, Application US/09095855 Patent No. 6160093 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Diskette
IBM Compatible
                                                                                                                                                                                                              Ouery Match
Best Local Similarity 49.7...
Thos 90; Conservative
                                                                                             ORGANISM: Verticillium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                 ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(30)
US-09-177-234-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDALL
STREET: 2001
THW: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-095-855-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 S 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 A 194
                        SEQ ID NO 6
                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

Fri Jan

```
APPLICANT: Stinner, Margot
APPLICANT: Scott, Linda
APPLICANT: APPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGRNT INFORMATION:
NAME: Sleath, Janet
REGISTATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LESGSANACPDAILLIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 RPLGRETPTPMPPRVADHVAAVVVFG--NPLRDIRGGGPRLEPR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 11.9%; Score 119; DB 2; Best Local Similarity 31.1%; Pred. No. 6.7e-05; Matches 51; Conservative 21; Mismatches 52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compounds and Methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPBRATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 154, Application US/09095855 Patent No. 6160093 GENERAL INFORMATION:
                                            Hiyama, Jun
Visser, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Stinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-095-855-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
US-08-997-362-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . vo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                        Sequence 154, Application US/08997080
Patent No. 596854
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAM, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
132 RPLGRFTPTPMPPRVADHVAAVVVFGNPLRDIRGGGPLPQMSGTYGPKSIDLCALDDPFC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 -----SELSGAVKEQVKGVALFGYTQNLQN-RGGIPNY-PR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/997,080 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: APPLICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.9%; Score 119; DB 2;
31.1%; Pred. No. 6.7e-05;
tive 21; Mismatches 52
                                                                                                                                     164 TGTLIITPAHLSYT----IEARGEAARFLR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11000.1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 154, Application US/08997362 Patent No. 5985287 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFRENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2601 E1
CITY: Seattle
STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-08-997-080-154
                                                                                                                                                                                                                                                                                                                                    US-08-997-080-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-997-362-154
                                                                                                                                                                                                                                                                                                 RESULT 7
g
                                                                                    ò
                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
```

S

12;

40;

```
TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVGE---QSVG----TYA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 IPTASADPCPDIEVIFARGTGAEPG-LG-WVGDAFVNALRPKVGE---QSVG----TYA 76
                                                                                                                                                                                                                                                                                                                                                                     9 LESGSANACPDAILLIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JEAULICANT: Watson, James D.

APPLICANT: Watson, James D.

APPLICANT: Watson, James D.

APPLICANT: Watson, James D.

TITLE OF INVENTION: Compounds and Methods for Treatment and TITLE OF INVENTION: Diagnosis of Mycobacterial Infections

FILE REFERENCE: 11000.1002c4

CURRENT PELLOR DATE: 1908-1002c4

CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: 09/095,855

EARLIER FILING DATE: 1998-06-1108

EARLIER FILING DATE: 1997-06-1108

EARLIER FILING DATE: 1997-06-12

EARLIER FILING DATE: 1997-06-13

EARLIER FILING DATE: 1997-06-12

SAFINER FILING DATE: 1997-06-12

WUMBER OF SEQ ID NOS: 208

WUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                    Ouery Match 11.9%; Score 119; DB 4; Length 748; Best Local Similarity 31.1%; Pred. No. 6.7e-05; Matches 51; Conservative 21; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SELSGAVKEQVKGVALFGYTQNLQN-RGGIPNY-PR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SELSGAVKEQVKGVALFGYTQNLQN-RGGIPNY-PR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 119; DB 4;
Pred. No. 6.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.9%; Score 119; Ub
31.1%; Pred. No. 6.7e
tive 21; Mismatches
     NUMBER OF SEQ ID NOS: 194
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 154
LENGTH: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 154, Application US/09205426 Patent No. 6406704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium vaccae
                                                                                                                        ORGANISM: Mycobacterium vaccae FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.11
Matches 51; Conservative
                                                                                                                                                                                              ; LOCATION: (119)...(119)
US-09-324-542-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (119)...(119)
US-09-205-426-154
                                                                                                                                                                       NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
US-09-205-426-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 154
                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Watson, James D.
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000.1007c1
CURRENT APPLICATION NUMBER: US/09/324,542
EARLIER FILING DATE: 1999-06-02
EARLIER FILING DATE: 1999-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.9%; Score 119; DB 4; Length 748; Best Local Similarity 31.1%; Pred. No. 6.7e-05; Matches 51; Conservative 21; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 -----SELSGAVKEQVKGVALFGYTQNLQN-RGGIPNY-PR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 RPLGRETPTPMPPRVADHVAAVVVFG--NPLRDIRGGPRLEPR 173
                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
                                                                      ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c3
TELECOMNINICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 154, Application US/09324542
Patent No. 6328978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/873,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
linear
                                                                                                                                                                                                                                                Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206-269-0563
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
US-09-095-855-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-324-542-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
```

12;

q

```
6
                  APPLICANT: Scott, Linds
APPLICANT: Scott, Linds
APPLICANT: Prestidge, Ross
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Visser, Margot
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION WIMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TNF-----LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.6%; Score 116; DB 2;
Best Local Similarity 30.1%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/997,362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11000.1002c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 -----SELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 RPLGRFTPTPMPPRVADHVAAVVVFG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 112, Application US/09095855 Patent No. 6160093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 112: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
         Skinner, Margot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 167 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 206-269-0563
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-997-362-112
                                                                                                                                                              STREET: Zov.
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                     98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-095-855-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                            Sequence 112, Application US/08997080

Patent No. 596854
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 TNF-----LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 167
132 RPLGRFTPTPMPPRVADHVAAVVVFG--NPLRDIRGGGPRLEPR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.6%; Score 116; DB 2; 30.1%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 30.1%; Pred. No. 1.6e-
Matches 44; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11000.1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 -----SELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 112, Application US/08997362
Patent No. 5885287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Hiyama, Jun
APPLICANT: Visser, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEPAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112:
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRNNDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-112
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98121
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                 RESULT 12
US-08-997-080-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-997-362-112
                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
```

ò g ò

```
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 112 LENGTH: 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: January 2, 2003, 15:07:05 Job time: 17 secs
                                                                   TYPE: PRT
ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                           11.68;
30.18;
                                                                                                                                                                                                                                                Best_Local Similarity 30.1%
Matches 44; Conservative
                                                                                                                                                          ; LOCATION: (119)...(119)
US-09-324-542-112
                                                                                                              FEATURE:
NAME/KEY: UNSURE
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Methods and Compounds for the Treatment TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders FILE REFERENCE: 11000.1007c1 CURRENT APPLICATION NUMBER: US/09/324,542 CURRENT FILING DATE: 1999-06-02 EARLIER APPLICATION NUMBER: US 08/997,080 EARLIER FILING DATE: 1997-12-23 NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.6%; Score 116; DB 4; Length 167; 30.1%; Pred. No. 1.6e-05; tive 19; Mismatches 47; Indels
                                                                                                                                                                                               SOFTWARE: PSSTEM: DOS
SOFTWARE: PSSTED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILLING DATE:
                  E: Law Offices of Ann W. Speckman
2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11000.1002c3
                                                                                                                                                                                                                                                                                                                            CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTONEY AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
TELECOMMUNICATION 10FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 ----SELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 112, Application US/09324542
Patent No. 6328978
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 112:
                                                                                                                                                                             E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 30.19
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-855-112
CORRESPONDENCE ADDRESS:
                                                                                                                                                      COMPUTER READABLE FORM:
                                         STREET: 2601 E
                                                                                                              USA
                                                                                                                               98121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-324-542-112
                                                                                     STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                Gaps
                                                                                             9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                     36;
;; Score 116; DB 4; Length 167;
;; Pred. No. 1.6e-05;
19; Mismatches 47; Indels
                                                                                                                                                                                                                  116 -----SELSGAVKEQVKGVALFG 133
```

ģ

THIS PAGE BLANK (USPTO)

H. insolens lipase
H. insolens mutant
H. insolens mutant
Mutant Humicola in
H. insolens mutant
Mutant Humicola in
Mutant Humicola in

```
Sutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsu1 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wild-type Humicola insolens mature cutinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
             AAR95051
AAB13705
AAB13711
                                                                                                                          AAB13716
AAB13709
ABB76830
ABB76836
                                                                                                                                                                                 ABB76843
ABB76846
                                                                                                                                                                                                           AAB13708
ABB76828
ABB76832
AAB13718
                                                                                                                                                                                                                                                                   ABB76857
ABB76827
ABB76835
                                                                                                                                                                                                                                                                                                                                       AAB13712
AAB13714
                                                                                 ABB76834
ABB76831
                                                      ABB76829
                                                                      AAB13710
                                                                                                                                                                                                                                                                                                             AAB13719
                                                                                                                                                                                                                                                                                                                            ABB76833
                                                                                                                                                                                                                                                                                                                                                                                   AAB13713
                                                                                                                                                                                                                                                                                                                                                                                                            ABB76840
                                                                                                                                                                                                                                                                                                                                                                     ABB76841
                                                                                                                                                                                                                                                                                                                                                                                               ABB76847
                                                                                                             AAB13717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM48435 standard; protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humicola insolens strain DSM 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000DK-0000861.
2000DK-0001577.
2000DK-0001772.
2001DK-0000100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-2001; 2001WO-DK00350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glad SOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVOZYMES AS
WO200192502-A1.
                                                                                                                                                                                                                                                                                                             97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-2000; 24-NOV-2000; 219-JAN-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36-DEC-2001.
9991
9991
9990
9990
9989
9987
9984
9983
9983
9983
9977
9977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM48435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM48435
 H. insolens mutant
H. insolens mutant
Mutant Humicola in
Mutant Humicola in
H. insolens mutant
Mutant Humicola in
H. insolens mutant
H. insolens mutant
H. insolens mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wild-type Humicola
                                                                                          2, 2003, 15:01:13 : Search time 36 Seconds (without alignments) 718.073 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chance to have a result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              / SIDS2/yggdata/geneseqp-embl/AA198 .DAT:
/ SIDS2/yggdata/geneseqp-embl/AA199 .DAT:
/ SIDS2/yggdata/geneseqp-embl/AA2000 .DAT:
/ SIDS2/yggdata/geneseqp-embl/AA2001 .DAT:
/ SIDS2/yggdata/geneseqp-embl/AA2001 .DAT:
/ SIDS2/yggdata/geneseqp-embl/AA2002 .DAT:
/ SIDS2/yggdata/geneseqp-embl/AA2002 .DAT:
                                                                                                                                                                   999
1 QLGAIENGLESGSANACPDA.....SYTIEARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution
             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                       908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB13706
ABB16837
ABB16838
ABB16844
AAB13707
ABB16839
AAB13703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM48435
                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                     US-09-873-075A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104
104
104
104
104
104
104
104
                                                                                                  January
```

Mutant Humicola in H. insolens mutant H. insolens mutant Humicola in H. insolens mutant Humicola in Mutant Humicola in

Humicola

Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution of

WPI; 2002-216714/27.

2 4 4 3 7 4 9 1 0 1 0 1 0 1 0 1 0 1

Score

Result

H. Insolens mutant
H. insolens mutant
H. insolens mutant
Mutant Humicola in
Mutant Humicola in
Mutant Humicola in
H. insolens mutant
Mutant Humicola in
H. insolens mutant
Mutant Humicola in
H. insolens mutant
Mutant Humicola in

Scoring table:

Searched:

Database

Perfect score:

on:

Sequence:

```
Similarity
                                                                                                                                                                                     194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humicola insolens.
                                               Example 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200034450-A1
                                                                                                                                         temperatures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-1998;
                                                                                                                                                                                                                       Matches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB13706;
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
   g
                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                           The present sequence is the wild-type mature cutinase from Humicola insolens strain DSM 1800, which was used to generate mutant cutinases (see ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers.
                                                                                                                                                                                                             61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                     AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                        1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 60
amino acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                      Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn;
                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild-type Glu substituted by Gln"
                                                                                                                                                         Indels
                                                                                                                                     100.0%; Score 999; DB 23;
ilarity 100.0%; Pred. No. 3.4e-100;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                     H. insolens mutant cutinase, E179Q substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsui T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                           Disclosure; Page 36; 41pp; English
                                                                                                                                                                                                                                                                                                                                                AAB13715 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98DK-0001604.
98US-0111591.
99DK-0000330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0124671
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                  RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                           AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVO-NORDISK
                                                                                                                                                                                                                                                                                                                                                                                                                                         protein co-ordinate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-482424/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 179
                                                                                                                                             Best Local Similarity
Matches 194; Conserv
                                                                                                                    194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humicola insolens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                    Sequence
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                  AAB13715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abo M,
                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                              RESULT 2
AAB13715
셤
                                                                                                                                                                                                            ò
                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                  g
```

```
ö
                                                                                                                                                                                        cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                                                                                                                                                                                                                                                                                                                                                                 Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patent: US 5,827,719.
                                                                                                                                                                 Site-directed mutagenesis was carried out on wild-type Humicola insolens
Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn; protein co-ordinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Glu substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 996; DB 21;
Pred. No. 7.2e-100;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H. insolens mutant cutinase, E47K substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB13706 standard; Protein; 194 AA
                                                                                                                -; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.7%;
illarity 99.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98DK-0001604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0111591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGEAARFLRDRIRA 194
```

```
The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48435), which was used to generate mutant cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) ibers. Note: the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                                   Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution of amino acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QLGAIENGLESGSANACPDAILIFARGSTEPGNWGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 OLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIOGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Leu substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.6%; Score 995; DB 23; 99.5%; Pred. No. 9.3e-100; tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant Humicola insolens mature cutinase #12
                                                                                                                                                                                Matsui
                                                                                                                                                                              Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humicola insolens strain DSM 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB76838 standard; Protein; 194
                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page -; 41pp; English.
                                                        2000DK-0001577.
2000DK-0001772.
2001DK-0000100.
                                        2000DK-0000861.
    22-MAY-2001; 2001WO-DK00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 99.5
Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glad SOS,
                                                                                                                                        (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                   WPI; 2002-216714/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200192502-A1
                                                                                                 19-JAN-2001;
                                                                                                                                                                              Svendsen A,
                                        02-JUN-2000;
                                                            23-OCT-2000;
24-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                    cutinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                 Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) libers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                                                                                                    Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ote: the present sequence is not shown in the specification but is stived from the H. insolens wild-type cutinase sequence given in SEQ of patent: US 5,827,719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild-type Thr substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 995; DB 21;
Pred. No. 9.3e-100;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mutant Humicola insolens mature cutinase #11.
                                                                             Matsui T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key Location/Qualifiers
Misc-difference 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB76837 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humicola insolens strain DSM 1800
                                                                           Svendsen A,
                                                                                                                                                                                                                                 Claim 16; Page -; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.68;
99US-0124671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.5
Matches 193; Conservative
                                      (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fukuyama S,
                                                                                                               WPI; 2000-482424/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200192502-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  temperatures.
16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB76837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived
                                                                         Abo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB76837
```

g

ð

8

ò

g

ò qq

ò

ö

Gaps

ö

Indels

ö

Phe"

Length 194;

```
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Svendsen A, Glad SOS,
                                                                                                                                 (NOVO ) NOVOZYMES AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thermostability; enz
protein co÷ordinate.
                                                                                                                                                                       WPI; 2002-216714/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGEAARFLRDRIRA
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                194 AA;
                    WO200192502-A1
                                                                                          23-OCT-2000;
24-NOV-2000;
                                                                                                               19-JAN-2001;
                                                                                 02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000
                                         06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                         cutinase
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB13707;
                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Óλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                            The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48435), which was used to generate mutant cutinases (ABM5687-ABM587-ABM5685). Cutinases (RC 3.1...74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                        οŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                          Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution camino acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG
                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                       Length 194;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                   99.6%; Score 995; DB 23;
llarity 99.5%; Pred. No. 9.3e-100;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant Humicola insolens mature cutinase #18.
                                                                                                                       Matsui
                                                                                                                       ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB76844 standard; Protein; 194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humicola insolens strain DSM 1800
                                                                                                                     Fukuyama
                                                                                                                                                                                                            Claim 8; Page -; 41pp; English.
                                               2000DK-0000861.
2000DK-0001577.
2000DK-0001772.
2001DK-000100.
                             2001WO-DK00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glad SOS,
                                                                                                 (NOVO ) NOVOZYMES AS.
                                                                                                                                         WPI; 2002-216714/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 130
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cutinase; enzyme;
                             22-MAY-2001;
                                                                              19-JAN-2001;
                                                02-JUN-2000;
                                                          23-OCT-2000;
24-NOV-2000;
                                                                                                                     Svendsen A,
         06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                              Best Local Sim
Matches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB76844;
                                                                                                                                                                                           cutinase
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76844
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

```
The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48435), which was used to generate mutant cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligomers of poly(ethylene terephthalate), comprises a substitution amino acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
/note= "Wild-type Arg substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 995; DB 23;
Pred. No. 9.3e-100;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H. insolens mutant cutinase, E179X substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB13707 standard; Protein; 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page -; 41pp; English.
                                                                                                                                                                                                                                                                    2000DK-0000861.
2000DK-0001577.
2000DK-0001772.
2001DK-0000100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.68;
                                                                                                                                                                                                  22-MAY-2001; 2001WO-DK00350
```

of

ö

```
enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution of amino acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                  /note= "Wild-type His substituted by Tyr"
                              Mutant Humicola insolens mature cutinase #13
                                                                                                                                                                           Location/Qualifiers
                                                                                                               Humicola insolens strain DSM 1800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page -; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       2000DK-000861.
2000DK-0001577.
2000DK-0001772.
2001DK-0000100.
                                                                                                                                                                                                                                                                                                                                             22-MAY-2001; 2001WO-DK00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.5
Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glad SOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-216714/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 AA;
                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                              WO200192502-A1
                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-2000;
24-NOV-2000;
19-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Svendsen A,
                                                                                                                                                                                                                                                                                                        06-DEC-2001
                                                                      Cutinase;
                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB13703
ID AAB1
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
             NAME OF A COURT OF A C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patent: US 5,827,719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPYVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIXA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thermostability are useful since they can withstand higher processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                           /note- "Wild-type Glu substituted by Asn or Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 993; DB 21;
Pred. No. 1.5e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                Svendsen A, Matsui T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                             ner
Misc-difference 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page -; 79pp; English.
                                                                                                                                                                                                                                                                             98US-0111591.
99DK-0000330.
99US-0124671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.48;
                                                                                                                                                                                                                                        99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                Abo M. Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-482424/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 193; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
Humicola insolens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 194 · AA;
                                                                                                                                                     WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   temperatures.
                                                                                                                                                                                                                                                                           04-DEC-1998;
09-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                        03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                             16-MAR-1999;
                                                                                                                                                                                              15-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB76839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB76839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
ABB76839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

Matsui

ŝ

Fukuyama

```
ö
The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48435), which was used to generate mutant cutinases (ABB76827-ABB76857). Cutinases (EC 3.1...74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) is solved the present sequence.in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PYDAALATWFLPRGTSQANIDEGKRLFALANOKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AVKEQVKGVALFGYTQNLQNRGCIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QLGAIENGLESGSANACPDAILIFARGSTEPGNWGITVGPALANGLESYIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%; Score 993; DB 23; 99.5%; Pred. No. 1.5e-99; live 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB13703 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGEAARFLRDRIRA 194
```

ဖ

181 RGEAARFLRDRIRA 194

g

AAB13703;

```
AAB13704 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                     WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   temperatures.
                                                                                                     17-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2000
                                                                                                                                                                                                                                       Synthetic.
                                                                        AAB13704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Abo M,
               RESULT 10
                              AAB13704
                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysing to cyclic oligomers of poly(ethylene terephthalate) i.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the H. insolens wild-type cutinase sequence given in SEQ ID tent: US 5,827,719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIPNIWIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: the present sequence is not shown in the specification but is
                                                     Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn; protein co-ordinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.3%; Score 992; DB 21; Length 194; 99.5%; Pred. No. 2e-99;
                                                                                                                                                                                         /note= "Wild-type Arg substituted by Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                             H. insolens mutant cutinase, R51P substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2e-99;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Matsui
                                                                                                                                                    Location/Qualifiers
51
                                                                                                                                                                                                                                                                                                                                                                                                                Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Page -; 79pp; English.
                                                                                                                                                                                                                                                                                                         98DX-0001604.
98US-0111591.
99DK-0000330.
99US-0124671.
                                                                                                                                                                                                                                                                               99WO-DK00678
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity ... Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-482424/42.
                                                                                                                                                                                                                                                                                                                                                                                                                Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 AA;
                                                                                                                 Humicola insolens
                                                                                                                                                             Key
Misc-difference
                                                                                                                                                                                                                      WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               temperatures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patent:
                                                                                                                                                                                                                                                                             03-DEC-1999;
17-NOV-2000
                                                                                                                                                                                                                                                                                                          04-DEC-1998;
                                                                                                                                                                                                                                                                                                                        09-DEC-1998,
09-MAR-1999,
                                                                                                                                                                                                                                                                                                                                                     16-MAR-1999;
                                                                                                                                                                                                                                                  15-JUN-2000
                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           derived
                                                                                                                                                                                                                                                                                                                                                                                                              Abo M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
```

QQ οy g ò

NAME OF THE PROOF OF THE PROOF

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patent: US 5,827,719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Site-directed mutagenesis was carried out on wild-type Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                          Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn; protein co-ordinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QLGAIXNGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Wild-type Glu substituted by Asn or Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Leu substituted by Ile"
                                                               H. insolens mutant cutinase, E6X/L138I substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 991; DB 21;
Pred. No. 2.5e-99;
l; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsui T;
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Page -; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98DK-0001604.
98US-0111591.
99DK-0000330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.2%;
ilarity 99.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0124671
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-482424/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 AA;
                                                                                                                                                                                                                                                        Humicola insolens.
```

61 61

25-JUN-2002

ABB76845;

181

181

g οχ

61 121

g à g Synthetic.

```
The present sequence is that of an enzyme with lipolytic activity, derived from Humicola insolens DSM1800. The enzyme has a mol. wt. of about 10-21 kDa, a pl in the range of 709, a pH optimum of about 8 and has specificity towards short-chain lipid substrates. It can be used as a detergent additive, partic. in compsns. for laundry washing or
                                                                 YDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGA 121
                                                                                VKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEAR 181
                                                                                                                                                Isolated DNA encoding lipolytic enzyme - derived from Humicola insolens DSM1800, used partic. as detergent additive for laundry and dishwashing compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLGAIENGLESGSANACPDAILLFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 60
 LGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGP
                    2 VGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     lipase; detergent; dishwashing; laundry; short-chain lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 991; DB 17;
Pred. No. 3.5e-99;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= signal_peptide 36..246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36..246
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 52; 63pp; English.
                                                                                                                                                                                                                                                                                                                 AAR95051 standard; Protein; 246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sandal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-DK00427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.2%;
ilarity 99.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94DK-0001240
                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kofod LV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                GEAARFLRDRIRA 194
                                                                                                                                                                                                                  WPI; 1996-239493/24.
                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                  H. insolens lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aumicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT29401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kauppinen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9613580-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dishwashing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                 AAR95051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                              122
                                                                                                                                                                                                182
                                                                                                                                                                                                                                182
                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                 AAR95051
                                                                                                                                                                                                                                                                                                                                  δŽ
                                                                                                                                                             a
                                                                                                                                                                                                δŻ
                                                                                                                                                                                                                           g
                           q
                                                                 οy
                                                                                       g
                                                                                                                             Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48435), which was used to generate mutant cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.7.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis
                                                                                                                                                                                                                                                                                                                                                                 Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution of amino acid residues corresponding to positions of Humicola insolens
of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                              AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 991; DB 23; Length 194;
Pred. No. 2.5e-99;
1; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Wild-type Gln substituted by Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Leu substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ë
                                                                                                                                                                                                                                                                                                                                Mutant Humicola insolens mature cutinase #19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                ABB76845 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 Humicola insolens strain DSM 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fukuyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page -; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2000DK-000861.
; 2000DK-0001577.
; 2000DK-0001772.
; 2001DK-000100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-2001; 2001WO-DK00350.
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                               RGEAARFLRDRIRA 194
                                                                                                                                Glad SOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-216714/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200192502-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-OCT-2000; 24-NOV-2000; 219-JAN-2001; 2
```

02-JUN-2000;

06-DEC-2001

Svendsen A,

cutinase

ö

Gaps

ö

Indels

Length 246;

Sequence

Query Match

ω

```
16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2000
                                                    192;
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
            Sequence
                                                                                                                                                                                                                                                                                         AAB13711;
                                 Query Match
                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abo M,
                                           Best Loca
Matches
                                                                                                                                                                                                                  181
                                                                                                                61
                                                                                                                                  61
                                                                                                                                                                                               181
                                                                                                                                                                                                                                                 RESULT 14
   X S
                                                                        ŏ
                                                                                          g
                                                                                                                ŏ
                                                                                                                                 g
                                                                                                                                                       δ
                                                                                                                                                                          qq
                                                                                                                                                                                               ò
                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                              Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patemat: US 5,827,719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid \cdot
                               121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                      36 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 95
                                                                                                                                                                                                                                                       Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn; protein co-ordinate.
                    PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG
                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild-type Glu substituted by Lys"
                                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type Ala substituted by Pro"
                                                                                                                                                                                                                                    H. insolens mutant cutinase, A14P/E47K substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsui
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                       AAB13705 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page -; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0111591.
                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-DK00678
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98DK-0001604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0124671
                                                                                                                                                                                                                 (first entry)
                                                                                                  RGEAARFLRDRIRA 194
                                                                                                              216 RGEAARFLRDRIRA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-482424/42
                                                                                                                                                                                                                                                                                                Humicola insolens.
                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                         WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    temperatures
                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1999;
                                                                                                                                                                                                                17-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2000
                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                             AAB13705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abo M,
                                       96
                     61
                                                                                                   181
                                                                                                                                                     RESULT 13
                                                                                                                                                                AAB13705
                                                                                                                                                                         a
                    à
                                       염
                                                          οy
                                                                              g
                                                                                                                    QQ
                                                                                                   à
```

```
ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid \dot{}
                                                                                                                                                                                                                                                                                                     180
                                                                                   Gaps
                                                                                                                             9
                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                 Site directed mutagenesis; cutinase; mutant; mutein; substitution; thermostability; enzyme; lipolytic; fabric finishing; yarn;
                                                                                                                                                      1 QLGAIENGLESGSPNACPDAILIFARGSTEPGNMGITVGPALANGLKSHIRNIWIQGVGG
                                                                                                                                                                                                                                       1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                PYDAALAINFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG
                                                                                   ó
                                          Length 194;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild-type Glu substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild-type Asp substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H. insolens mutant cutinase, E47K/D63N substitution.
                                        Score 990; DB 21;
Pred. No. 3.2e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsui T;
                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB13711 standard; Protein; 194 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Page -; 79pp; English.
                                      99.18;
99.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98DK-0001604.
98US-0111591.
99DK-0000330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-DK00678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0124671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein co-ordinate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukuyama S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-482424/42.
                                                              Similarity
194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humicola insolens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200034450-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-1998;
09-DEC-1998;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-DEC-1999;
```

```
cutinase
                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                            Search co
   8
                                                                                                                                                                                                                                                                               οχ
                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                          ô
lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing
                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), comprises a substitution of
                                                                 Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ 2 of patent: US 5,827,719.
                                                                                                                                                                                                                                                                   PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSOGAALIAAAVSELSG 120
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                     9
                                                                                                                                                                              1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG 60
                                                                                                                                                                                         1 QLGAIENGLESGSANACPDAILIFARGSTEPGNWGITVGPALANGLKSHIRNIWIQGVGG
                                                                                                                                                          ö
                                                                                                                                 Score 990; DB 21; Length 194;
Pred. No. 3.2e-99;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Ala substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild-type Asn substituted by Asp'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsui T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutant Humicola insolens mature cutinase #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         ABB76829 standard; Protein; 194 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humicola insolens strain DSM 1800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fukuyama
                                                                                                                                  99.1%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-2000; 2000DK-0000861.
23-OCT-2000; 2000DK-0001577.
24-NOV-2000; 2000DK-0001772.
19-JAN-2001; 2001DK-0000100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-2001; 2001WO-DK00350
                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-2002 (first entry)
                                                                                                                                             Best Local Similarity 99.0
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                          RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glad SOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-216714/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Misc-difference 44
                                                                                                              194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200192502-A1
                                                         temperatures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Svendsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               ABB76829
                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                          61
  8888888888888
                                                                                                                                                                               ð
                                                                                                                                                                                                 g
                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                               g
```

```
ö
                                                                                                                      The present invention relates to wild-type mature cutinase from Humicola insolens strain DSM 1800 (AAM48435), which was used to generate mutant cutinases (ABB76827-ABB7687). Cutinases (EC 3.1.1.74) are lipolytic enzymes capable of hydrolysing the substrate cutin. The mutant cutinases have improved thermostability, and are used for enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the present sequence in not shown in the specification, but is derived from the wild-type cutinase sequence shown on page 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
acid residues corresponding to positions of Humicola insolens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%; Score 990; DB 23; 99.0%; Pred. No. 3.2e-99; iive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2, 2003, 15:05:20
                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     January
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                  194 AA;
                                                                       Claim 8; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   completed: .
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 192;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
```

THIS PAGE BLANK (USPTO)

```
GenCore version 5.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2003, 15:06:24; Search time 10 Seconds (without alignments) 367.659 Million cell updates/sec 105-999

Sequence: US-09-873-075A-1

Sequence: 1 QLGAIENGLESGSANACPDA.....SYTIEARGEAARFLRDRIRA 194

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum Match 0%

Maximum Match 100%

Post-processing: Minimum Match 100%

Listing first 45 summaries
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

Published_Applications_AA:*

Database

SUMMARIES

	Description	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 10, Appl	Sequence 14, Appl	Sequence 52, Appl	Sequence 56, Appl	Sequence 197, App	Sequence 154, App	112,	Sequence 18, Appl	Æ	Sequence 11920, A	Sequence 6668, Ap	Sequence 7, Appli	Sequence 8, Appli	Sequence 13704, A	_	Sequence 22, Appl
	ID	US-09-873-075A-1	US-10-114-116-1	US-10-114-115A-1	US-09-791-171-10	US-09-791-171-14	US-09-791-171-52	US-09-791-171-56	US-10-051-643-197	US-10-051-643-154	US-10-051-643-112	US-09-950-368-18	US-10-077-111-10	US-09-815-242-11920	US-09-738-626-6668	US-10-017-828-7	US-10-017-828-8	US-09-815-242-13704	US-09-815-242-10079	US-09-854-799-22
	DB	10	σ	σ	10	10	10	10	σ	σ	0	10	6	10	σ	12	12	10	10	10
	Query Match Length DB	194	255	255	217	219	226	262	285	748	167	200	1356	398	309	1008	1008	424	1293	1454
æ	Query Match	100.0	26.8	26.8	19.8	18.8	17.9	16.8	14.5	11.9	11.6	8.7	8.3	8.3	7.7	7.7	7.7	7.6	7.4	7.3
	Score	666	268	268	197.5	187.5	179	167.5	145	119	116.	86.5	83	82.5	76.5	76.5	76.5	97	74	73
	Result No.	-	7	m	4	S	ø	۲.	œ	σı	10	11	12	13	14	15	16	17	18	19

Sequence 26, Appl Sequence 0680, Appl Sequence 10252, A Sequence 193, Appl Sequence 13898, Appl Sequence 1328, Appl Sequence 262, Appl Sequence 262, Appl Sequence 29, Appl Sequence 3867, Appl Sequence 3867, Appl Sequence 3867, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 27, Appl Sequence 3867, Appl Sequence 27, Appl Sequence 3867, Appl Sequence 3867, Appl Sequence 3867, Appl Sequence 3867, Appl Sequence 3707, Appl Sequence 27, Appl Sequence 3707, Appl Sequence 3	Sequence 6665, Ap
US-09-854-799-26 US-09-738-626-6080 US-09-738-626-6080 US-09-811-132-193 US-10-007-693-65 US-09-841-132-193 US-09-815-242-13998 US-09-815-242-13998 US-09-925-299-819 US-09-738-626-6888 US-09-738-626-6888 US-09-738-626-4632 US-09-738-626-4632 US-09-738-626-4632 US-09-738-626-4632 US-09-738-626-4632 US-09-738-626-3686 US-09-738-626-3686 US-09-738-626-3867 US-09-748-107-4 US-09-748-626-3867 US-09-748-63867	US-09-738-626-6665
100 100 100 100 100 100 100 100 100 100	σ
1454 4241 4241 4241 1530 1530 1531 1144 1144 1144 1144 1144 1145 1145	516
	e.9
72223 609 609 7.1522223 7.00 7.00 600 600 600 600 600 600 600 600 600	67.5
00000000000000000000000000000000000000	45

ALIGNMENTS

RESULT 1 (S-09-873-075A-1 (S-09-873-075A-1 (S-09-873-075A-1 (S-09-873-075A-1 (GENERAL INFORMATION: APPLICANT: Schroder Glad, Sanne FILE PEFERENCE: 10038.200-05 CURRENT FILING DATE: 2001-06-01 NUMBER OF SEQ ID NOS: 10 SOFTWARE: PatentIn version 3.1 SEQ ID NO 1 LENGTH: 194 CURRENT FILING DATE: 2001-06-01 SEQ ID NO 1 LENGTH: 194 CURRENT FILING LANGER OF OF MATCHE BEST LOCAL Similarity 100.0%; Prematches 194; Conservative 0; Matches 194; Conservativ
--

ö

```
188 ASKISSVLLFG---DPYKGKALPNVDASRVHTVCHAGDTICENSVIILPAHLTYAVDVAS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR PELING DATE: 1997-04-02
PRIOR FILING DATE: 1997-04-102
PRIOR FILING DATE: 1997-14-10
PRIOR FILING DATE: 1997-14-10
PRIOR FILING DATE: 1997-14-18
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/040,488
PRIOR FILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/09791171
Patent No. US/0020094336A1
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN Rikke
APPLICANT: RESTINGER, THOMAS
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                   Sequence 10, Application US/09791171 Patent No. US20020094336A1
                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELESN, Rikke
APPLICANT: OFTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 YTIEA-RGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YVQSGMTSQAATFAANRL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                  US-09-791-171-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-791-171-14
                                           183 EA 184
                                                                                 245 AA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-791-171-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196
    g
                                           δ
                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οŽ
                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 NFLPRGTSQANIDEGKRLFALANQ-----KCPNTPVVAGGYSQGAALIAAAVSELSGAV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 KEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 NFLPRGTSQANIDEGKRLFALANQ-----KCPNTPVVAGGYSQGAALIAAAVSELSGAV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 NGFTGACTDYTVLFARGISEPGNVGVLVGPPLAEAFEGAVGASALSFQGVNG-YSASV-E 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 KEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARG 182
                                                                                                                                                                                                                                                                                                                                                                                                                               20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 SGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALAT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 SGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALAT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                       Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.8%; Score 268; DB 9; Length 255
Best Local Similarity 34.6%; Pred. No. 1.1e-19;
Matches 63; Conservative 30; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sumitomo Chemical Co. Ltd.
TITLE OF INVENTION: Esterase Genes and Use thereof
FILE REFERENCE: P150409
CURRENT APPLICATION NUMBER: US/10/114,115A
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 09/585,468
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 1
                                                                        GENERAL INFORMATION:
APPLICANT: Sumitomo Chemical Co. Ltd.
TITLE OF INVENTION: Esterase Genes and Use thereof
FILE REFERENCE: P150409
CURRENT APPLICATION NUMBER: US/10/114,116
CURRENT FILING DATE: 2002-04-03
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                   26.8%; Score 268; DB 9; 34.6%; Pred. No. 1.1e-19; iive 30; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10114115A Patent No. US20020173013A1
                                     Sequence 1, Application US/10114116
Patent No. US20020164727A1
                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Aspergillus flavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Aspergillus flavus US-10-114-115A-1
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 34.68
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-114-115A-1
                                                                                                                                                                                                                                                                                   LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EA 184
RESULT 2
JS-10-114-116-1
                                                                                                                                                                                                                                                                                                                                             US-10-114-116-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                              SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
68 TNFLP----RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 VNYPASDDYRASASNGSDDASAHIQRTVASCPNTRIVLGGYSQGATVIDLSTSAMPPAVA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQVKGVALF----GYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIITPAHLS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ------VGGRSIGVYA 76
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.8%; Score 197.5; DB 10; Length 217; 30.8%; Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88;
```

11;

```
76 SQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAA----VSELSGAVKEQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                             126 VKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCT-GTLIITPAHLSYTI 178
                                                                                                                                                                                                                                                                                                                              71 LP-RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL--IAAAV-----SELS 119
                                                                                                                                                                                                                                                                                                    17 CPDAILLIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAALATNFLPRGT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OFTTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: RASMUSSEN, Peter Birk
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Malter
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NOCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT PILLING DATE: 2001-02-20
PRIOR FILLING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 ANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVG---GPYDAALATNF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ADGCPDAEVTFARGTGEPPGIG-RVGQAFVDSLR-----OQTGMEIGVYPVNYAASR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 262;
                                                                                                                                                                                                     Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 16.8%; Score 167.5; DB 10; Length Best Local Similarity 32.1%; Pred. No. 1.5e-09; Matches 68; Conservative 22; Mismatches 67; Indels
                                                                                                                                                                                                   17.9%; Score 179; DB 10; 32.5%; Pred. No. 8.4e-11;
                                                                                                                                                                                                                                                    24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR PILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-56
                                                                                                 ; TYPE: PRT; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/09791171 Patent No. US20020094336A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56
LENGTH: 262
                                                                                                                                                                                                                                                    63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ANDERSEN, Peter
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.
SEQ ID NO 52
LENGTH: 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 EARGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 GMTNQAARFVASRI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 173
                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-791-171-56
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                 APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
FRIOR APPLICATION NUMBER: 03/050,739
FRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-04-02
PRIOR FILING DATE: 1997-04-02
PRIOR PLILING DATE: 1997-04-02
PRIOR PLILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SUFFWARE PARCETING VOTO: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 ATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EQVKGVALFGYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIIT--- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAAL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NIELSEN, FIKE
APPLICANT: OETTINGER, Thomas
APPLICANT: OETTINGER, Thomas
APPLICANT: RASMUSSEN: Peter Birk
APPLICANT: ROSENKRANDS, Ide
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: WELDINGH, Karin
APPLICANT: PETER CONTINUED FOR MILE
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: 0F102.202.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.8%; Score 187.5; DB 10; Length 219; 31.7%; Pred. No. 1.1e-11; tive 32; Mismatches 75; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --PAHLSYTIEARG---EAARFLRDRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 NWPOHLAGAYVSSGMVNQAADFVAGKLQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR APPLICATION NUMBER: 1277/97
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/044,624
PRIOR APPLICATION NUMBER: 60/004,624
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium tuberculosis
US-09-791-171-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 52, Application US/09791171 Patent No. US20020094336A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.70,
  WELDINGH, Karin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ANDERSEN, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-791-171-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

13;

55; Gaps

```
SEQ ID NO 112
                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: Of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.100802
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR PLICATION NUMBER: US/9/156,181
SPION APPLICATION NUMBER: US/9/156,181
PRIOR PLICATION NUMBER: US/9/156,181
PRIOR PLICATION NUMBER: US/9/15/12/3
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: LAMPLICANTON TO 197
LENGTH: LAMPLICANTON TO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
150 AAYADNVAAVAVFG---NPSNRAGGSLSSLSPLFGSKAIDL-CNPTDPIC------H 196
                                                                                                                120 GAVKEQVKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCTGTLIITPAH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 TNF------LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SELSGAVKEQVKGVALFGY-TQNLQNRGGIPNYP---RERTKVFCNVGDAVC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 RPLGRFTPTPMPPRVADHVAAVVVFGNPLRDIRGGGPLPQMSGTYGPKSIDLCALDDPFC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-051-643-154

Sequence 154, Application US/10051643

Publication No. US20020197265A1

GENERAL INFORMATION:
APPLICANT: Watson, James D.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.1008c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.5%; Score 145; DB 9; Length 285; Best Local Similarity 28.6%; Pred. No. 3e-07; Matches 60; Conservative 31; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                               : | | | | | | 1.1| | 197 VGPGNEFSGHIDGYIPTYTTQAASFVVQRLRA 228
                                                                                                                                                                                                                                                                174 LSYTIEARG------EAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : : ||| :| || || SPGFNL-PAHFAYADNGMVE---EAANFAR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 TGTLIITPAHLSYT----IEARGEAARFLR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/051, 643 CURRENT FILING DATE: 2002-01-18 PRIOR APPLICATION NUMBER: US09/156,181 PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 197, Application US/10051643
Publication No. US20020197265A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-051-643-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-10-051-643-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                      엄
                                                                                                                ŏ
                                                                                                                                                                                      සු
                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
```

```
Sequence 112, Application US/10051643

Publication No. US20020197265A1

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Watson, James D.

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory

TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory;

TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory;

TITLE OF INVENTION: OF IMMUNER: USING MACOBACTERIUM VACCAB

FILE REFERENCE: 11000.100862

CURRENT APPLICATION NUMBER: US092-01.18

PRIOR APPLICATION NUMBER: US092/156,181

PRIOR APPLICATION NUMBER: US092/156,181

PRIOR APPLICATION NUMBER: US092-12-23
                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TNF-----LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 TNF-----LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LESGSANACPDAILLIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                    40;
                                                                                                                                                                                                                                                                                                                                                   Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 -----SELSGAVKEQVKGVALFGYTQNLQN-RGGIPNY-PR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 RPLGRFTPTPMPPRVADHVAAVVVFG--NPLRDIRGGGPRLEPR 173
                                                                                                                                                                                                                                                                                                                                                Query Match 11.9%; Score 119; DB 9; Best Local Similarity 31.1%; Pred. No. 0.00044; Matches 51; Conservative 21; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 11.6%; Score 116; DB 9; Similarity 30.1%; Pred. No. 0.00013; 44; Conservative 19; Mismatches 47
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----SELSGAVKEQVKGVALFG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 RPLGRETPTPMPPRVADHVAAVVVFG 157
                                                                                                                                                                                     ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium vaccae
                                                                                                                                                                                                                                       ; NAME/KEY: UNSURE
; LOCATION: (119)...(119)
US-10-051-643-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (119)...(119) US-10-051-643-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-10-051-643-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
```

S

```
QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                               Qγ
                                                                                           g
                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 DAALAT----NFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAV--- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 -SELSGAVKEQ----VKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVG--DAVCTGTLI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 KDVLKGAILHHPWVPIRGI------ELPDMAGLP------VFIGAGKYDPLCTK--- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VIAVGYSNGANIAASLLFHY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 GAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: beta transducin-like protein encoded by the OTHER INFORMATION: het-e-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                          GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
FILE REFERENCE: GC511-PCT
CURRENT APPLICATION NUMBER: US/09/950,368
CURRENT APPLICATION NUMBER: 09/355,166
PRIOR FILING DATE: 1999-07-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                        8.7%; Score 86.5; DB 10; 23.3%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.3%; Score 83; DB 9;
22.2%; Pred. No. 4;
tive 22; Mismatches 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/10077111
| Publication No. US20020187492A1
| GENERAL INFORMATION:
| APPLICANT: Todderud, C. Gordon
| APPLICANT: Finger, Joshua N. TITLE OF INVENTION: TBA IN:
| TITLE OF INVENTION: TBA IN:
| FILE REFERENCE: 3063-4114US2
| CURRENT FILIANG DATE: 2002-02-15
| PRIOR APPLICATION NUMBER: 60/269,181
| PRIOR PILING DATE: 2001-05-29
| PRIOR PILING DATE: 2001-05-29
| PRIOR FILING DATE: 2001-05-16
| NUMBER OF SEQ ID NOS: 25
| SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLVVRTRELKDFIDEAAETHQFNRGR-------
                                         Sequence 18, Application US/09950368 Patent No. US20020061580A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 ITPAHLSYTIEARGEAARFLRD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------EESEELYRYLRD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Podospora anserina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 22.2%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Bacillus
US-09-950-368-18
RESULT 11
US-09-950-368-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-077-111-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

Gaps

24;

73; Indels

```
'n
                                                                                      1123 ASGTCTQTLEGHGGWVHSVAFSPDGQRVASGSIDGTIKIWDAASGTCTQTLEGHGGWVQS 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 LFITTEEVGSGAAGALPWDVSEF------VGIDIAP-VAEGQNSNEHSVSVAMQDSG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| |: : | | : : | : : | : : | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : 
                                                                                                                                                                                                                             ANOKCPNTPVVAGGYSQGAALIAAAVSELSGAVKEQVK--GVALFGYTQNLQNRGG---- 143
39 GPALANGLESHIRNIW-----IQGVGGPYDAALATNFLPRG--TSQANIDEGKRLFAL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LGAIENGLESGSANACPDAILLIFARGSTEPGNMGITVGPALANGLES--HIRNIWIQGVG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John D.
APPLICANT: Tawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.3%; Score 82.5; DB 10; 26.7%; Pred. No. 0.92; tive 22; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1183 VAFSPDGQRVASGSSDKTIKIWDTASGTCTQTL 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ELITRALOLIS
CURRENT PEDELICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-67
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASLESEQ for Windows Version 4.0
SOFTWARE: FASLESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 -----IPNYPRERTKVFCNVGDAVCTGTL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11920, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.3%
Best Local Similarity 26.7%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 GAVKEQVKGVA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 GYERTHIDSLA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-815-242-11920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-738-626-6668
```

```
; ORGANISM: Homo sapiens US-10-017-828-7
                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/10017828

Sequence 7, Application US/10017828

Patent No. US20020119479A1

GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: METHODS FOR TREATING OR IDENTIFYING A
TITLE OF INVENTION: THE PRESENCE OF A VARIANT GPIIIA AND/OR VARIANT GPIIB ALLELE
FILE REFERENCE: 50211/01503
CURRENT APPLICATION NUMBER: US/10/017,828
CURRENT APPLICATION NUMBER: 09/409,648
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSED for Windows Version 4.0

SOFTWARE: FastSED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 CPAVEVIAAPGTWESAANDDPINPT-ANPLSFMLSITQPLOERYSADDVKVWTL---PY 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 DAALAT------NFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL-- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 -IAAAVSELSGAV-KEQVKGVALFGYTQNLQNRGGIPNYP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.7%; Score 76.5; DB 9; Best Local Similarity 19.5%; Pred, No. 2.7; Matches 42; Conservative 25; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 QPIVPGATMRGGRAGGFGVLNDRVQDICAPNDAIC 256
                                                         GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MAZOGULI, HIROSHI
APPLICANT: MAZOGULI, HIROSHI
APPLICANT: MAZOGULI, HIROSHI
APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KRIKO
APPLICANT: YOKOI, HARUHKO
APPLICANT: TATELSHI, NAOKO
APPLICANT: TATELSHI, NAOKO
APPLICANT: TEDA, MASATO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKHIRO
APPLICANT: SENOH, AKINO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFRENCES: 249-125
CURRENT APPLICATION NUMBER: US 99/377484
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SED ID NOS: 7059
SOFTWARE: PATECATION NUMBER: JP
SECTION NUMBER: JB
SECTION OF 6688
LENGTHRES
LENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 CPDAILIFARGSTEPGNMGITVGPALANGLESHIR--
Sequence 6668, Application US/09738626
Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Corynebacterium glutamicum
US-09-738-626-6668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-017-828-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠Ş
```

```
11;
                                                                                                                                                                                                                                                               631 LDSGEDDVCVPOLQLTASVTGSP----LLVGADNVLELOMDAAN---EGEGA-YEAELAV 682
                                                                                                                                                                                 Gaps
                                                                                                                                                              69 NFLPRGT----SQANIDEGKRLFALANQKCPN-TPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                                        124 EQVK-GVALFGYTQNLQNRGGIPNYPRE-RTKVFCNVGDAVCTGTLIITPAHLSYTIEAR 181
                                                                              9 LESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALAT 68
                                         35;
  Length 1008;
                                         Indels
    DB 12;
                                       32; Mismatches 71;
Score 76.5; 1
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: January 2, 2003, 15:10:16 Job time: 11 secs
Ouery Match

7.7%;

Best Local Similarity 24.6%;

Matches 45; Conservative 35
                                                                                                                                                                                                                                                                                                                      182 GEA 184
                                                                                                                                                                                                                                                                                                                                                         783 GNS 785
```

us-09-873-075a-1.rpr

```
January 2, 2003, 15:04:24; Search time 20 Seconds (without alignments) 932.504 Million cell updates/sec
                                                                                                                                                                                    US-09-873-075A-1
999
1 QLGAIENGLESGSANACPDA.....SYTIEARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                              283224
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                      Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	crip	cutinase (EC 3.1	_	· fu	E	(EC	cuti	_	probable cutinase	probable cutinase	probable cutinase		probable cutinase	conserved hypothet	hypothetical prote	endo-1,4-beta-xyla	bifunctional bioti	tyrocidine synthet	probable hemagglut	hypothetical prote		_	hypothetical prote				⊐	3-carboxy-cis,cis-	enterobactin synth	enterobactin synth
SUMMARIES	Ω	S20448	B27451	S21427	A27451	UVFUS	F70756	A70734	A70565	H70564	E70796	F70887	G70987	C86921	T35575	S13391	B82637	T31076	E83641	S76350	B86656	A69903	A95190	B98056	C83339	S71334	A83846	A87548	0	E85557
	DB	: -	~	Н	~	Н	ď	7	N	7	7	7	~	7	~	-	~	7	7	~	~	~	N	~	~	~	7	~	7	~
	Length	228	224	223	228	230	217	219	226	247	187	336	174	336	420	592	317	6486	3535	892	123	200	357	357	5627	302	338	382	1293	1293
dР	Query Match	. 0	ъ.	56.5	5	2	19.8	ъ.	7		11.5	10.3	•	•		8.9	•	•		•	٠.	•	•	٠.	8.6		8.4	٠.	8.3	8.3
	Score	601.5	584	564	558.5	553	197.5	187.5	179	167.5	114.5	103	86	95	88	88	88.5	88.5	88	87	86.5	86.5	98	98	98	84.5	83.5	83.5	83	83
	Result No.		7	٣	4	5	9	7	ω	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

beta transducin-li polyketide synthas	conserved hypothet beta-glucosidase f pristinamycin I sy endoglycosidase F3 hypothetical prote probable CoA trans probable histidino glutamate-1-semial hypothetical prote probable dehydroge probable multi-dom carboxy-terminal p carboxy-terminal p probable multi-dom	ALIGNMENTS	is it fungus) .0-Sep-1999 #text_change 10-Sep-1999	, B. a cutinase gene from Magnaporthe grisea 79; PMID:1557023	8; PIDN:CAA43717.1; PID:g1045205	re 601.5; DB 1; Length 228; d. No. 1.6e-45; Mismatches 50; Indels 1; Gaps 1	QLGAIENGLESGSANACPDAILJFARGSTEPGNWGITVGPALANGLESHIRN-IWIQGVG 59 ::	DAALATNELPRGTSQANIDEGKRLFALANOKCPNTPVVAGGYSQGAALIAAAVSELS 119 	ONLONRGGIPNYPRERTKVECNVGDAVCTGTLITFAHLSYTIE 179 		- anthracnose fungus (Colletotrichum gloeosporioides) Colletotrichum gloeosporioides vision 31-Mar-1989 #text_change 03-Mar-1994 Kolattukudy, P.E.
T18521 T30226	D83214 F97032 T30289 B46678 H84416 C83618 B702263 T36334 T36334 T36334 T37691	ALI(olast fungus (rice blast revision 10-	4448 . 232, 174-182, 1992 g and analysis of CUT1, a c Per: S20448; MUD:92212279; A448	7	Sco Pre 27;	IFARGSTI FARASGI	EGKRLFAI : EAKRMFTI	KEQVKGVALFGYTQNLQNRGGIPNYP! :: :		- anthracnose , Colletotrich evision 31-Mar ; Kolattukudy, 7 9 gene, CDNA, an
7 7			bla [re	G.; of IUID	2	. 28; . 08; e	AIL 	AID	ONR ONR		sor, ata, ere re
1356	2009 4 4 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8) - rice he grisea #sequence	ley, F. 174-182 malysis 0448; M	**************************************	60 60 ativ	SSANACPDAILI : SNAAACPSVILI	PRGTSQP PAGTTQC	FGYTONI FGYTKNI	RIRA 194 : QIRA 227	orecur singul equenc ral, S 7892, cutina
	mmm77110000000		the #s	thum 12, 13, 14, 15, 15, 15, 15, 15, 15, 15, 15, 15, 15	ATENTA SENTENTA	ırit mse	ESG:	NEI 	VAI -	RDF.	-) 1a 1a 1b 183- 0f A9
ω ω	xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx		1 1 1 POI	S20448 T.A.; Chum tet. 232, ting and an tumber: S20	ces: GB	similarity 17; Conserv	ENGL! RNDL	ALAI : SP	VKG :	ARFI : I	1 1985 1451 7451 7451 1re
ထထ	82.5 82.5 82.5 82.5 82.5 87.7 79.5 79.5 79.5 79.5		3.	S2(tyr 1- 1- 1y:	al 11		GPY DPY	GAV - AAV) ARGEAARFLRDRIRA 	m D u m - 0 U B m
30	2645000000444444		RESULT 1 S20448 cutinase C;Species C;Date: 1	C; Accession: R; Sweigard, C; Mol. Gen. Ger A; Title: Clor A; Reference r A; Accession:	A, Molecule A, Molecule A, Residues: A, Cross-ref C, Genetics: A, Gene: C, Superfami C, Keywords:	Query Ma Best Loc Matches	Qy 1 Db 33	Qy 60 Db 93	Oy 120 Db 153	Qy 180 Db 213	RESULT 2 B27451 cutinase (EC 3.1) F C'Species: Glomeralla of C'Date: 31-Mar-1989 #se C'Accession: B27451 R'Ettinger, W.F.; Thuka B10chemistry 26, 7883-7 A'Title: Structure of A'Reference number: A99 A'Accession: B27451

```
184 AARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APRFLAARI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: B00731
                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Ascoclyta rable:
C; Species: Ascoclyta rable:
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: S21427
R; Tenhaken, R.; Barz, W.
Submitted to the EMBL Data Library, April 1992
A; Description: Characterization and cloning of cutinase from Ascochyta rabiei.
A; Reference number: S21427
A; Sacession: S21427
A; Sacession: S21427
A; Sacession: S21427
A; Sesidues: pre-liminary
A; Molecule type: DNA
A; Residues: 1-223 <TEN>A; Cross-references: EMBL:X65628; NID:g2472; PIDN:CAA46582.1; PID:g2473
C; Genetics: A; Introns: 63/3
C; Superfamily: cutinase
                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             April 1992 cloning of cutinase from Ascochyta rabiei.
                                                                                                                                                                                                                                                                                                                       65 ALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKE 124
                                                                                                                                                                                                                                                                                                                                                                       125 QVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGEA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 EQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGE 183
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                      95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                  7 NGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLES--HIRNIWIQGVGGPYDA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 IENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESH-IRNIWIQGVGGPYD 63
                                                                                                                                                                                                                                                      ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 223;
            A,Residues: 1-224 <ETT> C.Comment: The cleavage site for the signal peptide is unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.5%; Score 564; DB 1; Length 22 58.6%; Pred. No. 3.1e-42; ive 29; Mismatches 48; Indels
                                                                                                                                                                                                    47; Indels
                                                            Ajntrons: 63/3
C;Superfamily: cutinase
C;Keywords: hydrollase
E;46-194,129-187/Disulfide bonds: #status predicted
F;96,136,204/Active site: Asp, Ser, His #status predicted
                                                                                                                                                                 58.5%; Score 584; DB 2;
59.0%; Pred. No. 5.4e-44;
iive 28; Mismatches 47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
S21427
cutinase - fungus (Ascochyta rabiei)
                                                                                                                                                                                 Best Local Similarity 59.0
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ||: :| |
APEFLKSKIGA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARFLRDRI 192
A; Molecule type: DNA
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                              C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
A27451
                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

```
cutinase (EC 3.1.-.-) precursor - fungus (Fusarium solani)
C; Species: Fusarium solani f.sp. pisi
C; Species: Fusarium solani f.sp. pisi
C; Date: 17-May-1985 *sequence_revision 17-May-1985 *text_change 11-Jun-1999
C; Accession: A32836; A00731; B00731; A6141.
J; Bacteriol. 171, 1942-1951; 1989
A; Title: Structure of the cutinase gene and detection of promoter activity in the 5'-A; Reference number: A32836; MUID:89197761; PMID:2703464
A; Residues: 1-47, 'A', 49-93, 'A', 95-230 <SOl>
A; Cross-references: GB:M29759; NID:9168147; PIDN:AAA33335.1; PID:9168148
A; Rossidues: 1-47, 'A', 49-93, 'A', 95-230 <SOl>
A; Cross-references: GB:M29759; NID:9168147; PIDN:AAA33335.1; PID:9168148
A; Rosiduey: C.L.; Flurkey, W.H.; Ookita, T.W.; Rolattukudy, P.E.
Proc. Natl. Acad. Sci. U.S.A. 81, 3339-3343, 1984
A; Title: Cloning and structure determination of cDNA for cutinase, an enzyme involved A; Reference number: A00731
                  - anthracnose fungus (Colletotrichum capsici) (fragme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in
                                                                                                                                                                                                                                derived amino acid sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
cutinase (EC 3.1.-.-) precursor - anthracnose fungus (Colletotrichum capsici C; Species: Colletotrichum capsici C; Species: Colletotrichum capsici C; Species: 13-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 30-Sep-1993 C; Accession: A27461
R; Ettinger, W.F.; Thukral, S.K.; Kolattukudy, P.E.
Biochemistry 26, 7883-7892, 1987
A; Title: Structure of cutinase gene, CDNA, and the derived amino acid sequen A; Reference number: A90524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fungal cutinase, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-230 <SSO2>
A; Cross-references: GB:K02640; NID:g168145; PIDN:AAA33334.1; PID:g168146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 NGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESH--IRNIWIQGVGGPYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 ALATNF-LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 EQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                           A Accession: A27451
A; Molecule type: DNA
A; Molecule type: DNA
B; Molecule type: DNA
A; Molecule type: DNA
C; Comment: The cleavage site for the signal sequence is not known.
C; Genetics:
A; Introns: 66/3
C; Superfamily: cutinase
C; Superfamily: cutinase
C; Keywords: hydrolase
F; 49-198,129-191/Disulfide bonds: #status predicted
F; 99,140,208/Active site: Asp, Ser, His #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 57-94;113-142;183-192 <SO3>
R; Soliday, C.L.; Kolattukudy, P.E.
Biochem. Biophys. Res. Commun. 114, 1017-1022, 1983
A; Title: Primary structure of the active site region of A; Reference number: A61421; MUID:83308716; PMID:6412706
A; Accession: A61421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 55.9%; Score 558.5; DB 2; Best Local Similarity 57.7%; Pred. No. 9.6e-42; Matches 109; Conservative 27; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 113-142 <SO4>
```

us-09-873-075a-1.rpr

```
L Similarity
66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: cutinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-226 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rv2301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
            124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                            Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
               ð.
                                                                                                                                  Óγ
                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
R:Lin, T.S.; Kolattukudy, P.E.

Bur. J. Biochem. 106, 341-351, 1980
A:Title: Structural studies on cutinase, a glycoprotein containing novel amino acids and A:Reference number: A44665; WUID:80245930; PMID:739618
A:Contents: annotation; identification of glucuronylated amino end C;Comment: This enzyme catalyzes the hydrolysis of cutin, a polyester that forms the str C;Comment: Southern blot results suggest that the genome contains two copies of the cutin C;Genetics:
A:Introns: 64/3
A:Introns: 64/3
A:Introns: 64/3
B:32-32-30/Product: cutinase #status predicted <SIG>F:1-31/Domain: signal sequence #status predicted <SIG>F:1-31/Domain: cutinase #status predicted <ARAT>
F:32-30/Product: cutinase #status predicted <ARAT>
F:32/Modified site: glucuronylated amino end (GIy) (in mature form) #status experimental F:125-187/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable cutinase precursor with N-terminal signal sequence - Mycobacterium tuberculosis (Species: Mycobacterium tuberculosis (C) Species: Mycobacterium troposis (C) Species: Mycobacterium troposis (C) Species (C) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
Residues: 1-217 <COL>
Cross-references: GB:274025; GB:AL123456; NID:g3261586; PIDN:CAA98399.1; PID:g1403471
Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: |: |: || 77 VNYPASDDYRASASNGSDDASAHIQRTVASCPNTRIVLGGYSQGATVIDLSTSAMPPAVA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGGPYDAALAINFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSGAVKEQVKGVALFGYTQNLQNRGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFLP----RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QLG-AIENGLESGSANACPDAILLIFARGSTEPGNMGITVGPALANGLESH1--RNIWIQG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.8%; Score 197.5; DB 2; 30.8%; Pred. No. 4.7e-10; iive 26; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 553; DB 1;
Pred. No. 3e-41;
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||| | || :::||
PDARGPAPEFLIEKVRA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 55.33
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:Z7-A;Experimental source: st
C;Genetics:
A;Gene: Rv1984c
C;Superfamily: cutinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
probable cutinase precursor - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
R;Cole, S.T.; Brosch, R.; Parkhill, T.; Gentles, S.; Harris, D.; Gordon
R;Cole, S.T.; Brosch, J.; Ritter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genc
A;Reference number: A70509; MUID: 98295987; PMID: 9634230
A;Actus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: GB: 277163; GB: AL123456; NID: 93261610; PIDN: CAB00997.1; PID: 94493
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whitehead, S.; Barrell, B.G. tuberculosis from the complete geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: 295390; GB: AL123456; NID: 93261766; PIDN: CAB08718.1; PID: 921043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holroyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aviotable cutinase precursor - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: A70565
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Halure 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70565
A;Status: preliminary; nucleic acid sequence not shown; translation not shown B. Mesianes: 1-206 A;Coles
                                              --NQIDVGAN----DMSAHIQSMAN-SCPNTRLVPGGYSLGAAVTDVVLAVPTQMWGFTN 133
EQVKGVALF-----GYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIITPAHLS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 ATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 PLPPGSDEHIAAVALFG--NGSOWVGPITNFSPAYNDRTIEECHGDDPVCHPADPNTWEA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAAL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 GAVAPATAACPDAEVVFARGRFEPPGIG-TVGNAFVSALRSKVNKNVGVYAVKYPAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----EQVKGVALFGYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIIT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.8%; Score 187.5; DB 2; 31.7%; Pred. No. 3.6e-09; ive 32; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NWPQHLAGAYVSSGMVNQAADFVAGKLQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --PAHLSYTIEARG---EAARFLRDRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain H37Rv C; Genetics:
                                                                                                                                                             176 YTIEA-RGEAARFLRDRI 192
                                                                                                                                                                                                                                          YVQSGMTSQAATFAANRL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
```

9

```
Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandram, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A.Reference number: A70500; MUID:98295987; PMID:9634230
A.Accession: E70796
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.Resiques: 1-187 <COL>
A.COSS-references: GB.AL022121; GB:AL123456; NID:93261559; PIDN:CAA18046.1; PID:9296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricole, Str.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Balandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.7Hille: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A.Reference number: A7050; MUID:98295987; PMID:9634230
A.Steference number: A7050; MUID:98295987; PMID:963250
A.Steference number: A7050; MUID:98295987; PMID:963250
A.Steference number: A7050; MUID:98295987; PMID:963256026; PIDN:CAA17866.1; PID:e125
A.Steperimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C; Accession: F70887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 RNIWIQGVGGPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 ------IAAAVSELSGAVKEQVKGVALFG--YTQNLQNRGGIP----NYPRE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGYVTSAVVPPAVPVQAVPAPMAPEVANHVAAVTLFGAPSAQFLGQYGAPPIAIGPLYQP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 YDAALATNFLPRGTSQANIDEGKRLFALA----NQKCPNTPVVAGGYSQGAALIAAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ACPDAILIFARGSTE------PGNMGITV-GPALANGLESHIRNIWIQGVGGP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Rv3802c - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKVECNVGDAVCTGTLIITPAHLSYTIEAR-GEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LS---GAVKEQ-VKGVALFGYTQNLQNRGG-IPNYPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 11.5%; Score 114.5; DB 2; Best Local Similarity 26.4%; Pred. No. 0.0078; Matches 43; Conservative 22; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.3%; Score 103; DB 2; 22.7%; Pred. No. 0.16; live 24; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                               C,Genetics:
A,Gene: Rv3724
C,Superfamily: cutinase
       C; Accession: E70796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: Rv3802c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
F70887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promate cutinase - Wycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: H70564
R;COle, S.T.; Brosch, R; Parkhill, J; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S. Rajanfream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUD: 98295987; PMID: 9634230
A;Accession: H70564
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-247 <COL>
A;Coss-references: GB: 295390; GB: AL;23456; NID: 93261766; PIDN: CABOR77.1; PID: 92104374
C;Genetics:
A;Gene: Rv4451
C;Superfamily: cutinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable cutinase precursor - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                  Gaps
                                                                                                                                                                                                          76 SQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAA----VSELSGAVKEQ 125
                                                                                                                                                                                                                                                                                                               126 VKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCT-GTLIITPAHLSYTI 178
                                                                                                                                                                                                                                                                                                                                                                                                               LP-RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL--IAAAV----SELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAVKEQVKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCTGTLIITPAH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                             17 CPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAALAINFLPRGT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 ANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVG---GPYDAALATNF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAYADNVAAVAVFG---NPSNRAGGSLSSLSPLFGSRAIDL-CNPTDPIC-----H
                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.8%; Score 167.5; DB 2; Length 247; 1larity 32.1%; Pred. No. 2.4e-07; Conservative 22; Mismatches 67; Indels 55
                                                                             Length 226;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable cutinase - Mycobacterium tuberculosis (strain H37RV)
                                                                       Query Match 17.9%; Score 179; DB 2; L
Best Local Similarity 32.5%; Pred. No. 2.1e-08;
Matches 63; Conservative 24; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | : | : | | WGPGNEFSGHIDGYIPTYTTQAASFVVQRLRA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSYTIEARG------EAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||||: ||
213 GMTNQAARFVASRI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 EARGEAARFLRDRI 192
A; Gene: Rv3452
C; Superfamily: cutinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
hes 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                               ö
                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

6

Qy 150ERTKVFCNVGDAVCTG-TLIITPAHLSYTI 178 	QY 59 GGPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL 110
RESULT 12 G70987 probable cutinase - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: G70987 R;Cole, S.T.; Barcsch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.	QY 111 IAAAVSELSGAVKEQ-VKGVALFGYTQNLQNRGGIPNYPRE
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 Nature Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. Natitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Mcference number: A70500; MUID:9829987; PMID:9634230 A; Mclecule Type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Mesidues: 1-174 < MOL> A; Mcross-references: GB:295890; GB:AL123456; NID:93242245; PIDN:CAB09321.1: PID:92131026	RESULT 14 T35575 hypothetical protein SC6G4.24 SC6G4.24 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 C;Accession: T35575 R;Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1998 A;Reference number: 221583
A:Experimental source: strain H37Rv C;Genetics: A;Gene: Rv1758 C;Superfamily: cutinase C;Superfamily: cutinase Query Match Best Local Similarity 29.9%; Pred. No. 0.2; Matches 52; Conservative 22; Mismatches 64; Indels 36; Gaps 12;	A; Accession: T35575 A; Status: preliminary: translated from GB/EMBL/DDBJ A; Status: preliminary: translated from GB/EMBL/DDBJ A; Status: preliminary: translated from GB/EMBL/DDBJ A; Residues: 1-420 A; Residues: 1-420 A; Cross-references: EMBL: ALO31317; PIDN: CAA20402.1; GSPDB: GN00070; SCOEDB: SCGG4.24 A; Experimental source: strain A3(2) C; Genetics: A; Gene: SCOEDB: SCGG4.24
OY 44 NGLESHIRNIWIQGVGGPYDAALATNFLPRGTSQANI-DEGRRLFALANQKCPNTFVV 100 1	Query Match 8.9%; Score 89; DB 2; Length 420; Best Local Similarity 26.9%; Pred. No. 3.4; Matches 36; Conservative 20; Mismatches 64; Indels 14; Gaps 5;
OY 101 AGGYSQGAALIAAAVSELSGAVKEQVKGVALFGYTQNLONRGGIP 145	QY 10 ESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNI-WIQGVGG 60
OY 146NYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGE-AARFLRDRI 192 :	QY 61 PYDAALATNFLPRGTSQANIDE-GKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELS 119 1
RESULT 13 C86921 Conserved hypothetical protein ML0099 [imported] - Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: Mycobacterium leprae C; Species: O-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001	OY 120 GAVKEQVKGVALFG 133 Db 221 DLVRERVVGVALVG 234 RESULT 15
P.R.; HC Holroyd,	S13391 endo-1,4-beta-xylanase (EC 3.2.1.8) B - Pseudomonas fluorescens subsp. cellulosa endo-1,4-beta-xylanase (EC 3.2.1.8) B - Pseudomonas fluorescens subsp. cellulosa C;Species: Pseudomonas fluorescens subsp. cellulosa C;Date: 17.Apr.1993 #sequence_revision 11-Apr.1997 #text_change 18-Jun-1999 C;Accession: S13391
	R;Kellett, L.E.; Poole, D.M.; Ferreira, L.M.A.; Durrant, A.J.; Hazlewood, G.P.; Gilbe Biochem. J. 272, 369-376, 1990 A;Title: Xylanase B and an arabinofuranosidase from Pseudomonas fluorescens subsp. ce A;Reference number: S13391; MUID:91097447; PMID:2125205 A;Accession: S13391 A;Molecule type: DNA A;Residues: 1-592 <kel>A;Assidues: 1-592 <kel>A;Cross-references: EMBL:X54523; NID:945523; PIDN:CAA38389.1; PID:945524</kel></kel>
	C.Genetics: A;Gene: xynB C.Gunction: A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans A;Pathway: xylan degradation C;Superfamily: Pseudomonas endo-1,4-beta-xylanase B; bacterial cellulose-binding doma C;Superfamily: Pseudomonas polysaccharide degradation C;Superfamily: bacterial cellulose-binding domain homology <bcb> F;38-134/Domain: bacterial cellulose-binding domain homology <bcb> F;337-592/Domain: Streptomyces endo-1,4-beta-xylanase A homology <sxy></sxy></bcb></bcb>

```
ira, L.M.A.; Durrant, A.J.; Hazlewood, G.P.; Gilbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDN:CAA20402.1; GSPDB:GN00070; SCOEDB:SC6G4.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B - Pseudomonas fluorescens subsp. cellulosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subsp. cellulosa
ion 11-Apr-1997 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                               ion 05-Nov-1999 #text_change 05-Nov-1999
                      RLFALANQKCPNTPVVAGGYSQGAALIAAAVSELS 119
--EGKRLFAL----ANQKCPNTPVVAGGYSQGAAL 110
                                                                           FGYTQNLQNRGGI--PNYPRE------ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | : : | |:| |:| OLKAVIDAAAPEGPIVLVGHSMGGMTVMALADAFP 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GITVGPALAN-----GLESHIRNI-WIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                    l, J.; Barrell, B.G.; Rajandream, M.A.
August 1998
                                                                                                                                                    VGDAVCTG----TLIITPAHLSYTIEARGE 183
                                                                                                                                                                               .24 - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            core 89; DB 2; Length 420; red. No. 3.4; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     rom GB/EMBL/DDBJ
```

Fri Jah

```
January 2, 2003, 15:01:33 ; Search time 12 Seconds (without alignments) 670.534 Million cell updates/sec
                                                                                                                                                                                           US-09-873-075A-1
999
1 QLGAIENGLESGSANACPDA.....SYTIEARGEAARFLRDRIRA 194
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SwissProt_40:*
                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                   Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			Descr	******************************
S				:
			Π	1
			DB	1
			Length	
	æ	Query	Match	111111
			Score	
				į

	Description	P41744 alternaria			P29292 ascochyta r			P00590 fusarium so	Q96ut0 fusarium so		P52956 aspergillus		mycobacte				O30409 b tyrocidin				006591 mycobacteri			Q40147 lycopersico	Q9x7b8 mycobacteri	P14859 homo sapien			_		O52765 salmonella	_	yed7	-
SOMMAKIES	OI.	CUTI_ALTBR	CUTI_MAGGR	CUTI_COLGL	CUTI_ASCRA	CUTI_COLCA	CUTI_FUSSC	CUT1_FUSSO	CUT2_FUSSO	CUT3_FUSSO	CUTI_ASPOR	CUTI_BOTCI	CUT1_MYCTU	CUT2_MYCTU	CUT3_MYCTU	XXNB_PSEFL	TYCC_BACBR	ENTF_ECO57	HET1_PODAN	EBA3_FLAME	HI81_MYCTU	GSA_SOYBN	MURD_ENTFA	GSA_LYCES	HIS8_MYCLE	OCT1_HUMAN	BACA_BACLI	Y370_RHIME	GATA_CAMJE	MURG_BACHD	SYH_SALTY	YPT1_CAEEL	RECF_BRUME	PM11_CHLPN
	B	1	Н.	П,	-	Н	Н	-	Н	Н	-	,	٦	П	П	Н	П	Н	Н	-	-	П	٦.	_	Н	-		-	_	Н	-	-	~	7
	Match Length	209	228	224	223	228	230	230	231	231	213	202	217	219	247	592	6486	1293	1356	329	380	466	456	481	377	743	5255	423	453	363	423	482	384	928
% Ouery	Match	60.5	60.2		٠.	'n.	ď.	S	2	4	4	ς.	6	ъ.	•	٠	٠		8.3	٠			7.9	7.9		٠	7.8	7.7	٠	7.6	7.6	7.6	7.6	7.6
	Score	604	601.5	584	564	558.5	558	553	520.5	548.5	445	226	197.5	187.5	167.5		88.5	83	83	82	81	80	78.5	- 1	78	^	77.5			92	92	7	75.5	
Result	No.	г	C (. 0	4"	n.	9	7	œ	o i	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P53711 paplo cynoc 099148 y bifunctio 052657 rickettsia P77552 escherichia P77552 escherichia P77554 escherichia P55409 rattus norv 02fec4 chlamydomon 089552 listeria mo P08993 trypanosoma P56300 canine enfe	TIS 9 AA.	P41744; 01-NoV-1995 (Rel. 32, Created) 01-NoV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Cutinase precursor (EC 3.1.1.74).	otina; Dothideomyoetes; : Pleosporaceae; Alternaria.	ter 1c plo 1ty	productics ere are as it. Usa the http:	1. NASE. IMILARITY. IMILARITY. IMILARITY. IMILARITY. IMILARITY.	DB 1; Length 209; 1.7e-44; Indels 2; Gaps 1;	QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGV 58 : :
ITAB_PAPCY PURZ_YARLI OMPA_RICCN YDHO_ECOLI ENTF_ECOLI ENTF_ECALI ENTF_ECALI ENTE_ECALI	ALIGNMENTS PRT; 209	ed) sequence upd annotation u 1.74).	a; Pezizomyc ; mitosporic	ENCE FROM N.A. C., Koeller W.; intted (NOV-1993) to the EMBL/GenBank/DDBJ dar FUNCTION: Catalyzes the hydrolysis of cutin, forms the structure of plant cuticle. Allows penetrate through the cuticular barrier into the initial stage of the fungal infection (Br CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin mon SUBCELLULAR LOCATION: Secreted. SIMILARITY: BELONGS TO THE CUTINASE FAMILY.	This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institutions as long as use by non-profit institutions as long as entities requires a license agreement (See http. or send an email to license@isb-sib.ch).	se. 2; 1. 2; 1. Signal. POTENTIAL. CUTINASE. BY SIMILARITY.	Score 604; D. Pred. No. 1.7. 22; Mismatches	LIFARGSTEPGNMG
ਜਿਕਜ਼ਾਜਜਜਜਜਜ -	-	eat st st	cot	the off	col tuti ics titi ent ent nse	inas. 1. 1. 1. SE 1. SE 2. SE 2. SE 2. SE 3. SE	86;	AIL-
604 788 2021 418 1293 429 495 1783 363 420 1451	ANDARD;	32, Cr 32, La 41, La	sicola. Ascomy osporac	ilyzes llyzes lcture sugh th lvITY: CCATIONGS	try is Instinformati It ins statem a lice	3470.1; finase: finase: furinase: curinase: curinase: curinase: curinase: 170 170 170 119 119 119	for the conservative	LESGSANACPD
CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	ST?	(Rel. (Rel. (Rel.	brassic Fungi; s; Plec 29001;	FROM N.A. Coeller W. (NOV-195) ION: Cate the strutate throught in the strute through in the strute through in the strute action in the structure	PROT er e Swiss n Bioir n-profi d this quires	3; AAAC 0; 1XZC 0; 1XZC 0; 1XZC 83; Cut 00129; C 00129; C 00129; C 108 108 119 119 174	ilarity Conser	NGLESGS
335 74.5 335 74.5 336 74.5 339 74.5 339 74.5 441 73.5 442 73.5 444 73.5	LT 1 _ALTBR · CUTI_ALTBR	P41744; 01-NOV-1995 01-NOV-1995 15-JUN-2002 Cutinase pr	Alternaria Eukaryota; Pleosporale; NCBI_TaxID-	SEQUENCE FROM N.A. Yao C., Koeller W.; Submitted (NOV-1993) to the Fruction: Catalyzes the forms the structure of penetrate through the the initial stage of the initial stage of the initial stage of the Initial stage of the SUBCELDUAR LOCATION:	This SWISS-PF between the the European use by non- modified and entities requ	EMBL; U03393; AAA04470.1; HSSP; P00590; IXZG. InterPro; IPRO00675; Cutinase. PFan; PF01083; Cutinase; 1 PROSITE; PS00129; CUTINASE. PROSITE; PS00155; CUTINASE. PROSITE; PS00931; CUTINASE. PROSITE; PS00931; CUTINASE. PYDROLASE; Serine esterase; S197 SIGNAL 7 209 CUTINASE. DISULFID 108 170 BY DISULFID 108 170 BX ACT_SITE 119 119 BY ACT_SITE 119 119 BY ACT_SITE 119 BY ACT_SITE 187 BY SEQUENCE 209 AA; 21648 MW; 1	Query Match Best Local Simila Matches 118; Co	1 QLGAIE)
	RESULT CUTI_A ID C	5 E D D B	0000 x		388888888		Qu. Be: Ma'	QY

```
CUTI_COLGL P11373;
                                                                                                                                                                                                                                                                                                                                         Glomerella
                                                                                                                                                                                                                                                                                                         cinqulata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                         CUTI_COLGL
                                                     09
           ~
                                                                                                                                                                                              RESULT
                             Db
                                                                                                                   Q
                                                                                                                                                             Д
                                                                                                                                                                                                                              δy
                                                     ŏ
                                                                       g
                                                                                             á
                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                Mol. Gen. Genet. 232:174-182(1992).
-!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that forms the structure of plant cuticle. Allows pathogenic fungi to penetrate through the cuticular barrier into the host plant during the initial stage of the fungal infection.
                                                                          SGAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
 QASTTRNELETGSSDACPRIIFIFARGSTEAGNMGALVGPFTANALESAYGASNVWVQGV 72
                    GGPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSEL
                                                                                                                                                                                                                                                                                                                                                   Sweigard J.A., Chumley F., Valent B.; "Cloning and analysis of CUT1, a cutinase gene from Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .N-LINKED (GLCNAC. . .) (POTENTIAL)
BBOACE063B9D4627 CRC64;
                                                                                                                                                                                                                                                          Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea). Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. NCBL_MaxID-148305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine esterase; Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60.2%; Score 601.5; DB 1 60.0%; Pred. No. 3.1e-44;
                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-TUN-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.11.74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUTINASE.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                  228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X61500; CAA43717.1; ALT_TERM.
                                                                                                                                                                                                                                                                                                                                       MEDLINE=92212279; PubMed=1557023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00129; CUTINASE.
PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000675; Cutinase. Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                   STANDARD;
                                                                                                         EARGEAARFLRDRI 192
                                                                                                                      || :| || :|
EAAVQAPTFLRAQI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228
196
189
138
193
206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             STRAIN=4091-5-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P00590;
                                                                                                                                                                                  CUTI_MAGGR
P30272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                        grisea.
Mol. Ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                              RESULT 2
CUTI_MAGGR
                                                                                                       179
 13
                                         73
                                                               119
                                                                                                                             193
                     59
g
                     δλ
                                         g
                                                               à
                                                                                  d
                                                                                                       ŏ
                                                                                                                           a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                 93 DPYDAALSPNFLPAGTTQGAIDEAKRMFTLANTKCPNAAVVAGGYSQGTAVMFNAVSEMP 152
                                                                                           GPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELS 119
                                                                                                                                                                                  120 GAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIE 179
                                                                                                                                                                                                          59
                        QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRN-IWIQGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-JUN-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CUTINASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                            224 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine esterase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; B27451; B27451.
HSSP, P00590; 1CUW.
InterPro; IPR00675; Cutinase.
Pfam; PF01083; Cutinase; I.
PRINTS; PR00129; CUTINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M21443; AAA33042.1; -.
                                                                                                                                                                                                                                                                                                                           227
                                                                                                                                                                                                                                                                             180 ARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                        213 SSIAAPNWLIRQIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5457;
```

```
PRINTS; PR00129; CUTINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUTI_COLCA
ID CUTI_COLCA
AC P10951;
      ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                   Query Match
            FT
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tenhaken R., Barz W.;
Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
- FUNCTION: Catalyzes the hydrolysis of cutin, a polyseter that
- FUNCTION: Catalyzes the hydrolysis of cutin, a polyseter that
forms the structure of plant cuticle. Allows pathogenic fungi to
penetrate through the cuticular barrier into the host plant during
the initial stage of the fungal infection (By similarity).
- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.
- SUBCELLULAR LOCATION: Secreted.
- INDUCTION: By contact with cutin.
- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                         ||:|||| ||| ||| ||:|| :|| ||| ||| ||:|| :|| ||| ||:|| :|| ||:|| :|| ||:|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 QVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGEA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 ALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKE 124
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                   7 NGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLES--HIRNIWIQGVGGPYDA 64
                                                                                                                                                                                                                                                                                      5;
                                                                                                                                Length 224;
                                                                                                                                                                                            47; Indels
                                                                   1C5BACEAB469ABFA CRC64;
                                                                                                                         58.5%; Score 584; DB 1; 59.0%; Pred. No. 9.4e-43; iive 28; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ascochyta rabiei.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
mitosporic Pezizomycotina; Ascochyta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.1.1.74)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CUTINASE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
      BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nastr

PinterPro; IPR000675; Cutinase.

Pfam; PF01083; Cutinase; 1.

PRINTS; PR00129; CUTINASE.

PROSITE; PS00155; CUTINASE.1; 1.

PROSITE; PS00931; CUTINASE.2; 1.

Hydrolase; Serine esterase; Signal.
   191 BY
204 BY
23477 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X65628; CAA46582.1; -.
                                                                                                                                                                                      Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
191 1
204 2
224 AA;
                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CBS 534.65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P00590; 1CUW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 ARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 PRFLQARI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUTI_ASCRA
P29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S21427
   ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUTI_ASCRA

ID CUTI_A

P29292

DT 01-DEC.

DT 15-JUN

DE CULIDAR

ON MID-TR

      FT
                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

STRAIN-ATCC 48574;

Ettinger W.F., Thukral S.K., Kolattukudy P.E.;

Ettinger W.F., Thukral S.K., Colattukudy P.E.;

Ettinger W.F., Thukral S.K., CDBN, and the derived amino acid

Structure of cutinase gene, CDBN, and the derived amino acid

sequence from phytopethogenic fungi.";

Bochemistry 26:7983-792(1987).

I Gorms the structure of plant cuticle, Allows pathogenic fungi to

penetrate through the cuticular barrier into the host plant during

the initial stage of the fungal infection.

COTALIVITY: Cutin + H(2)0 = cutin monomers.

COTALIVITY: Secreted.

INDUCTION: By contact with cutin.

COTALIVITY: By CONTACT with cutin.

PTM: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE

COTALIVITY: RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.

SEMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                                       124 EQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGE 183
                                                                                                                                                                                                                                                                                                                                                                                                         64 AALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                  5 IENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESH-IRNIWIQGVGGPYD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colletotrichum capsici (Anthracnose fungus).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
                                                                                                                                                                                                                     ä
                                                                                                                                                           Length 223;
                                                                                                                                                                                                                        Indels
                                                                                             1E82A5ADD1B5E7FB CRC64;
                                                                                                                                                       56.5%; Score 564; DB 1; LA 58.6%; Pred. No. 4.7e-41; ive 29; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cutinase precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M18033; AAA33043.1; --
PIR; A27451, A27451
HSSP, P00590; ICUW
INTERPRO; IPR000675; Cutinase.
Pfam; PF01083; Cutinase.
                                                                                             23520 MW;
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
   135
189
202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 APEFLKSKIGA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 AARFLRDRIRA 194
   135
189
202
223 AA;
                                                                                                                                                                                    Best Local Similarity
Matches 112; Conserv
```

Fri

```
X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
HSSP, P00590, 2CUT.
InterPro, IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
                                                                                 47
125
136
191
204
                                                                                                                                                                                                                                                                                                                                                                                                                  CUT1 OR CUTA
                                                                                                                                                                   Matches 110;
                                                                                                                                                                                                                                                                                                                                                             CUT1_FUSSO P00590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=T-8;
                                                                                                  ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                  DISULFID
                                                                                             DISULFID
                                                                                                                                                 Query Match
                                                                                                                                                           Local
                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                    CUT1_FUSSO
                                                                                                                                                                                                                                                                                                                                            RESULT 7
                                                                                                                                                           Best
  염
                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                          염
                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                            유
                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 ALATNF-LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                     EQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGE 183
                                                                                                                               Gaps
                                                                                                                                             7 NGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESH--IRNIWIQGVGGPYDA 64
                                                                                                                                                        <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                   Fusarium solani (subsp. cucurbitae) (Nectria ipomoeae).
Bukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
Hypocreales; Nectriaceae; Nectria.
NCBI_TaxID=57162;
                                                                                                          55.9%; Score 558.5; DB 1; Length 228; 57.7%; Pred. No. 1.4e-40;
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers. SUBCELLULAR LOCATION: Secreted.
                                                                                         3825D42C23DA139B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·! - SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
11-NOV-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.1.1.74).
                                  CUTINASE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                         230 AA.
                                                                                                                             27; Mismatches
                 Hydrolase; Serine esterase; Signal.
SIGNAL 1 16 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-PGB 153;
MEDLINE-97254998; PubMed-9100380;
CUTINASE_1; 1.
CUTINASE_2; 1.
                                  228 C 198 B 191 B 140 B 195 B 208 C 23714 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U63335; AAB05922.1; -.
                                                                                                                             Conservative
                                          49
129
140
195
208
228 AA;
                                                                                                                  Best Local Similarity
Matches 109; Conserv
PS00155; PS00931;
                                                                                                                                                                                                                                                         184 AARFLRDRI 192
                                                                                                                                                                                                                                                                          219 APRFLAARI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       CUTI_FUSSC
Q99174;
                                                            ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
PROSITE;
                                           DISULFID
                                                                                                            Query Match
                                     CHAIN
                                                                                                                                                                                                                                                                                                      RESULT 6
CUTI_FUSSC
ö
                                                                                                                                                              a
                                                                                                                                                                                 ò
                                                                                                                                                                                                  8
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                        q
```

```
58 VGGPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 LSGAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter activity in
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soliday C.L., Flurkey W.H., Okita T.W., Kolattukudy P.E.; "Cloning and structure determination of cDNA for cutinase, an enzyme involved in fungal penetration of plants."; proc. Natl. Acad. Sci. 0.5.A. 81:3939-3943(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Martinez C., de Geus P., Lauwereys M., Matthyssens G., Cambillau C., "Fusarium solani curtinase is a lipolytic enzyme with a catalytic series accessible to solvent.";
Nature 356:615-618(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QLG-AIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusarium solani (subsp. pisi) (Nectria haematococca).
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreales, Nectriaceae, Nectria.
                                                                                                                                                                                                                                                                                                                                                                                   51; Indels
                                                                                                                                                                                                                                                                                         05FB3C33326405AA CRC64;
PRINTS; PR00129; CUTINASE.
PROSITE; PS00129; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
Hydrolase; Serine esterase; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soliday C.L., Dickman M.B., Kolattukudy P.E.;
"Structure of the cutinase gene and detection of
the 5'-flanking region by fungal transformation."
J. Bacteriol. 171:1942-1951(1999).
                                                                                                                                                                                                                                                                                                                                                             1.6e-40;
                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cutinase 1 precursor (EC 3.1.1.74).
                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230 AA.
                                                                                                                          BY SIMILARITY.
CUTINASE.
                                                                                                                                                                                                                                                                                                                                                                                   32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                          Score 558;
                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=89197761; PubMed=2703464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92220194; PubMed=1560844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                         23902 MW;
                                                                                                                                                                                                                                                                                                                                   55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||| | || :::||
209 PDARGPAPEFLIEKVRA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 IEARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                 194
187
136
191
204
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                      230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
```

э; Э

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: Secreted.
-:- INDUCTION: By contact with cutin.
-:- PTM: THE 2 DISULFIDE BONDS PLAT & CRITICAL ROLE IN HOLDING THE CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME.
-:- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
            Martinez C., Nicolas A., van Tilbeurgh H., Egloff M.-P., Cudrey Verger R., Cambolilau C.; "Cutinase, a lipolytic enzyme with a preformed oxyanion hole."; Biochemistry 33:83-89(1994).
                                                                                                                                                                                                                                                                                                                      Prompers J.J., Groenewegen A., van Schaik R.C., Pepermans H.A.M.
Hilbers C.W.;
                                                                                            X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS).
MEDLINE=97318923: PubMed=9175860;
Longhi S., Czjzek M., Lamain V., Nicolas A., Cambillau C.;
"Atomic resolution (1.0 A) crystal structure of Fusarium solani cutinase: stereochemical analysis.";
                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.15 ANGSTROMS) OF 33-230. Nicolas A., Martinez C., Cambillau C.; Submitted (MAR-1997) to the PDB data bank.
                                                                                                                                                                                                                                                                                                        MEDLINE=98046750; PubMed=9385640;
MEDLINE=94114517; PubMed=8286366
                                                                                                                                                                                    J. Mol. Biol. 268:779-799(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; K02640; AAA33334.1; -. EMBL; M29759; AAA33335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1005; 31.701.94.
1007; 31.701.96.
1008; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 11.701.96.
1009; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A32836; A32836.
                                                                                                                                                                                                                                                                       [7]
STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
PIR;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
PDB;
                                                                                                                                                                                                    (9)
```

```
Li D., Strakova T., Rogers L., Ettinger W.F., Kolattukudy P.E.;
"Regulation of constitutively expressed and induced cutinase genes by
different zinc finger transcription factors in Fusarium solani f. pisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSGAVKEQVKGVALFGYTQNRQIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 VGGPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QLG-AIENGLESGSANACPDAILLIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Serine esterase; Glycoprotein; Signal; 3D-structure.
SIGNAL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusarium solani (subsp. pisi) (Nectria haematococca).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 553; DB 1; Length 230; Pred. No. 4.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     R -> A (IN REF. 2).
R -> A (IN REF. 2).
7253ACAA657AD1AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
cutinase 2 precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                          GLUCURONIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.4%; Score 553; 55.3%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                             CUTINASE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypocreales; Nectriaceae; Nectria.
                                                                                                                                                                                                                                                               PRINTS; PR00129; CUTINASE.
PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
                                                                                                                                                                                                                                 InterPro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23982 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||| | || :::||
209 PDARGPAPEFLIEKVRA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEARGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                           230
32
194
187
136
191
                                                         1XZE; 14-OCT-96.
1XZE; 14-OCT-96.
1XZG; 14-OCT-96.
1XZH; 14-OCT-96.
1XZH; 14-OCT-96.
              .4-OCT-96.
.4-OCT-96.
.4-OCT-96.
                                                                                                                                       14-OCT-96.
30-NOV-96.
                                                                                                                                                                                                                  GlycoSuiteDB; P00590;
                                                                                                                                                                     1XZL; 30-NOV-96.
1XZM; 30-NOV-96.
                                                                                                                                                                                                    01-APR-98
                                                                                                                                                                                                                                                                                                                                                                          47
125
136
191
204
48
94
230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=70791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUT2_FUSSO
Q96UT0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-T-8;
                                                                                                                                                                                                      1AGY;
                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUT2_FUSSO
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
```

us-09-873-075a-1.rsp

```
(Haematonectria haematococca).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 RGPAPEFLIEKVRA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUTI_ASPOR
P52956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sest Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUTI_ASPOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
  SOUTH THE TENT TO THE SOUTH THE TENT TO THE SOUTH THE TENT THE TEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
;
           Li D., Sirakova T., Rogers L., Ettinger W.F., Kolattukudy P.E.; "Regulation of constitutively expressed and induced cutinase genes by different zinc finger transcription factors in Fusarium solani f. pisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusarium solani (subsp. pis1) (Nectria haematococca).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.
SIMILARITY.
8047714A249CB756 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 550.5; DB 1
Pred. No. 6.8e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CUTINASE 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cutinase 3 precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Serine esterase; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nectriaceae; Nectria.
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF417004; AAL18696.1; -.
InterPro: IPR00675; Cutinase.
PEdm; PF01083; Cutinase.
PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
(Haematonectria haematococca).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23932 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || | | || :::||
RGPAPEFLIEKVRA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231
195
188
137
192
205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGEAARFLRDRIRA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=70791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypocreales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUT3_FUSSO
Q96US9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=T-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUT3_FUSSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
```

ŏ g δ 셤 δ g ò g HER REPARENTED TO THE SECONDARY OF THE SECONDARY SECONDA

```
between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ć
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 GTTRNDLTNGNSASCADVIFIYARGSTETGNLG-TLGPSIASKLESAFGRDGVWIOGVGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohnishi K., Toida J., Nakazawa H., Sekiguchi J.;
"Genome structure and nucleotide sequence of a lipolytic enzyme gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB39E3EBECDED202 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          le-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-ocr-1996 (Rel. 34, Created)
01-ocr-1996 (Rel. 34, Last sequence update)
01-Cr-LUN-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.11.74) (L1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.2%; Pred. No. 1e-3 ive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 548.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUTINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Serine esterase; Signal SIGNAL 1 16 POTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=IFO.4202;
MEDLINE=95220642; PubMed=7705606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF417005; AAL18697.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24016 MW;
```

~

```
penetrate through the cuticular barrier into the host plant during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 226; DB 1;
Pred. No. 2.1e-12;
27; Mismatches 84
                                                                                                                                                     SIMILARITY: BELONGS TO THE CUTINASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CUTINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Serine esterase; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=H37Rv;
MEDLINE-98295987; Pubmed-9634230;
                                                                                                                                                                                                                                                                                                                                                                               Interpro: IPR000675; Cutinase.
Pfan; PP01083; Cutinase; 1.
PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS00931; CUTINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20253 MW;
                                                                                                                                                                                                                                                                                                                                               EMBL; Z69264; CAA93255.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
106
117
169
182
202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-1773;
                                                                                                                                     SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 RGEAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 TAAAA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUT1_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      010837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUT1_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
             FEMS Microbiol. Lett. 126:145-150(1995).
-!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that forms the structure of plant cuticle. Seems, in this nonpathogenic fungl, to play an important role in flavor formation.
-!- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 SQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKEQVKGVALFGYT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 CPDAILIFARGSTEPGNMGITVGPALANGLE-SHIRNIWIQGVGGPYDAALATNFLPRGT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 CKPITFIFARASTEPGLLGISTGPAVCNRLKLARSGDVACQGVGPRYTADLPSNALPEGT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>
ن
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Botryotinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2213317B4A14A0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 445; DB 1;
Pred. No. 5.6e-31;
); Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
01-SUN-2002 (Rel. 41, Last annotation update)
Cutinase precursor (EC 3.1.1.74).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Botrytis cinerea (Botryotinia fuckeliana).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CUTINASE.
                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00129; CUTINASE.
PROSTIE; PS00155; CUTINASE_1; 1.
PROSTIE; PS001931; CUTINASE_2; 1.
Hydrolase; Serine esterase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000675; Cutinase. Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22263 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.5%;
50.3%;
                                                                                                                                                                                                                                                                                                                           EMBL; D38311; BAA07428.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
of Aspergillus oryzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=40559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUTI_BOTCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUTI_BOTCI
ID CUTI_B
AC 000298
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
CO CUTIA...
CO CO HEICTION
CO NOBI_T
RN ISLO
RN SEQUEN
RN SEQUEN
RN SEQUEN
RN SEQUEN
RN SEQUEN
RN SECUEN

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as ison as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAD---VPGFL-QGGDPAGSQTMATMVTSTLSSCPDTKLVISGYSQGGQLVHNAAKLLPA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEA 180
the initial stage of the fungal infection (By similarity).

CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
SUBCELLULAR LOCATION: Secreted (By similarity).

PTW: THE 2 DISULFIDE BONDS PLAY A CRITICAL ROLE IN HOLDING THE
CATALYTIC RESIDUES IN JUXTA-POSITION; REDUCTION OF THE DISULFIDE
BRIDGES RESULTS IN THE COMPLETE INACTIVATION OF THE ENZYME (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--*RNIWIQGVGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                031D64725A23D8E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-Dubable cutinase Rv1994c precursor (EC 3.1.1.74).
RV1984C OR MT2037 OR MTCX39.35.
```

ŝ

```
RESULT 13
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Bropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                               STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                        s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 INFLP----RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 VNYPASDDYRASASNGSDDASAHIQRTVASCPNTRIVLGGYSQGATVIDLSTSAMPPAVA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQVKGVALF ---- GYTQNLQNRGGIPNYP --- RERTKVFCNVGDAVCTGTLIITPAHLS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical and
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd (Hornsby T., Jagels K., Krooph A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculist; Nu1984c; ...
InterPro; IPR000675; Cutinase.
InterPro; IPR000379; Ser_estrs_site.
PROSITE; PS01083; Cutinase; 1.
PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; COORDIST CUTINASE_2; 1.
Hypothetical protein; Hydrolase; Serine esterase; Signal; Complete proteome.
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE CUTINASE RV1984C.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500589547B9A87B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 5.9e
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.8%; Score 197.5; 30.8%; Pred. No. 5.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE007056; AAK46312.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 YTIEA-RGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YVQSGMTSQAATFAANRL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z74025; CAA98399.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32
217
184
177
1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
193
217 AA;
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcdon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Davies R., Devlin K., Chillingworth T., Connor R., Davies R., Devlin K., Krogh A., McLean J., Moule S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Squares S., Squares R., Shelton S., Shancel B.G.; Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L. Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBL_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00155; CUTINASE_1; 1. PROSITE; PS00931; CUTINASE_2; FALSE_NEG. Hypothetical protein; Hydrolase; Serine esterase; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- SIMILARITY: BELONGS TO THE CUTINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F7678DD0D1E127A8 CRC64;
                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable cutinase Rv2301 precursor (EC 3.1.1.74).
RV2301 OR MT2358 OR MTCY339.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
PROBABLE CUTINASE R
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                     219 AA.
                                                                                                                                                                                                                                                                           MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tuberculist; Rv2301; -.
InterPro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22598 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z77163; CAB00997.1; -.
                                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE007078; AAK46643.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
                   STANDARD;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P00590; 1CEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112
178
196
219 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; MT2358; -
               CUT2_MYCTU
Q50664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
CUT2_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
```

Length 219;

DB 1;

Score 187.5;

18.8%;

Query Match

```
DISULFID
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                             Best Local
                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
XYNB_PSEFL
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                              염
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Dodboy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaewa M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-9825987; pubmed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglimeier K., Gas S., Barry C.E. III, Frekaie F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence.";
                                                                                                      ----- EQVKGVALFGYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLIIT--- 170
                                                                                                                                                           134 PLPPGSDEHIAAVALFG--NGSQWVGPITNFSPAYNDRITELCHGDDPVCHPADPNTWEA 191
                                                                                         ATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAAVSELSGAVK 123
              35; Gaps
                                       GLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAAL 66
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                               25 GAVAPATAACPDAEVVFARGRFEPPGIG-TVGNAFVSALRSKVNKNVGVYAVKYPAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
 4.2e-09;
ches 75;
                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable cutinase Rv3451 precursor (EC 3.1.1.74).
RV3451 OR MT3557 OR MTCY13E12.04.
                                                                                                                                                                                                                                                                                      247 AA.
             Conservative 32; Mismatches
  .
02
                                                                                                                                                                                                           --PAHLSYTIEARG---EAARFLRDRIR 193
  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z95390; CAB08717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE007160; AAK47897.1;
                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CDC 1551 / Oshkosh;
                                                                                                                                                                                                                                                                                      STANDARD;
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                   CUT3_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bishai W.;
  Local
                                                                                                                                                                                                                                                            RESULT 14
CUT3_MYCTU
                                                                                         29
                                                                                                                 81
                                                                                                                                           124
                                                                                                                                                                                             171
              Matches
                                       ω
                                                                                                                                                                                                                                                                                      ð
                                                              g
                                                                                          à
                                                                                                                g
                                                                                                                                           ö
                                                                                                                                                                  용
                                                                                                                                                                                          ò
                                                                                                                                                                                                                  셤
```

```
LP-RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL--IAAAV-----SELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAVKEQVKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCTGTLIITPAH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 AAYADNVAAVAVFG---NPSNRAGGSLSSLSPLFGSKAIDL-CNPTDPIC-----H 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kellett L.E., Poole D.M., Ferreira L.M.A., Durrant A.J.,
Hazlewood G.P., Gilbert H.J.;
"Xylanase B and an arabinofussidase from Pseudomonas fluorescens
subsp. cellulosa contain identical cellulose-binding domains and are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 ANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVG---GPYDAALATNF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- PATHWAY: Hemicellulose degradation.
-i- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 ADGCPDAEVIFARGTGEPPGIG-RVGQAFVDSLR-----QQTGMEIGVYPVNYAASR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYDROLASES).
SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
(CBD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - FUNCTION: XYLANASE B CONTRIBUTES TO HYDROLYSE HEMICELLULOSE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAJOR COMPONENT OF PLANT CELL-WALLS.
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 â
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-3UN-2002 (Rel. 41, Last annotation update)
Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase (1,4-beta-D-xylan xylanohydrolase B).
                                                               PROSITE; PS00155; CUTINASE_1; 1.
PROSITE; PS0031; CUTINASE_2; FALSE_NEG.
Hypothetical protein; Hydrolase; Serine esterase; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    67; Indels
                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C -> L (IN REF. 2).
C -> D (IN REF. 2).
W; 07804671A066D5FF CRC64;
                                                                                                                                                                         PROBABLE CUTINASE RV3451.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 167.5; DB 1
; Pred. No. 2.4e-07;
.22; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     592 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 39-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 VGPGNEFSGHIDGYIPTYTTQAASFVVQRLRA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 LSYTIEARG------EAARFLRDRIRA 194
                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Sp. Cellulosa;
MEDLINE-91097447; PubMed-2125205;
Tuberculist; Rv3451; -.
InterPro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded by adjacent genes.";
Biochem. J. 272:369-376(1990).
                                                                                                                                                                                                                                                                                                                                                               24884 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       16.8%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas fluorescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linkages in xylans.
                                                                                                                                                           26
247
1180
1173
1177
1191
22
                                                                                                                                                                                                                                                                                                                                                             247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                110
177
191
22
194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XYNB_PSEFL
                                                                                                                                                                                CHAIN
DISULFID
                                                                                                                                                                                                                                              ACT_SITE
ACT_SITE
ACT_SITE
CONFLICT
CONFLICT
SEQUENCE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 ATNFLPRGTSQANIDEG--KRLFALANQKCPNTPVVAGGY-------SQGAA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 NACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPY-DAAL----- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Gaps
                                                                                                                            EMBL: X5453; CAA38389.1;
PIR; S13391; S13391
HSSP: P07986; LEXG.
InterPro: PR001019; Bac_celose-bind.
InterPro: IPR001019; Bloc_hydro_10.
Pfam; PF00331; Glyco_hydro_10; 1.
Prinrs; PR00134; GLHYDRIASE10.
PROSITE; PS00591; GLYCOSYL_HYDRO_F10; 1.
PROSITE; PS00561; GBD_BACTERIAL; 1.
Cellulose degradation; Xylan degradation; Hydrolase; Glycosidase;
                                                                                                                                                                                                                                                                                                                                ENDO-1,4-BETA-XYLANASE B.
CELLUUCOSE-BINDING (BY SIMILARITY)
SER-RICH (LINKER).
SER-RICH (LINKER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 LIAAAVS--ELSGAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match '8.9%; Score 89; DB 1; Length 592; Best Local Similarity 24.9%; Pred. No. 2.8; Matches 43; Conservative 19; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                           PROTON-DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                       63410 MW;
                                                                                                                                                                                                                                                                                                                     38
134
160
320
330
530
                                                                                                                                                                                                                                                                                                                                                                                                                                       592 AA;
                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                  Signal.
SIGNAL
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
```

Search completed: January 2, 2003, 15:05:39 Job time: 13 secs

```
2, 2003, 15:04:04; search time 30 Seconds (without alignments) 1332.438 Million cell updates/sec
                                                            1 QLGAIENGLESGSANACPDA......SYTIEARGEAARFLRDRIRA 194
                                                                                             671580
    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                           Total number of hits satisfying chosen parameters:
                                                                                   671580 seqs, 206047115 residues
                                                                                                                              summaries
                       - protein search, using sw model
                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                     sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_hage:*
                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su
                                                                                                      length: 0
length: 2000000000
                                                                                                                                            sp_archea:*
sp_bacteria:*
                                                  US-09-873-075A-1
999
                                                                                                                                        SPTREMBL_21:*
                                                                                                      Minimum DB seq
Maximum DB seq
                                                  Title:
Perfect score:
                                                                     Scoring table:
                       OM protein
                                                            Sequence:
                                                                                   Searched:
                                                                                                                                        Database
                                Run on:
```

Ogpci3 xylella fas 09171 pseudomonas 05567 synechocyst 05567 synechocyst 05676 synechocyst 05676 synechocyst 05046 lactococcus 09041 arcaptcoccus 097120 pseudomonas 09120 triboderma 09120 helicobacte 08120 heli

16 09PCI3 16 091791 16 091791 2 09WXI8 16 034645 2 09ED94 16 09YXI1 16 09YXI1 16 09YXI1 16 09YI2 16 09HD01 2 09ED60 16 09ED60

3317 3535 966 1976 11976 11976 11931 12737 1317 12737 1317 12737 1317 1 ALIGNMENTS

0914W3 0931V7 088VE1 08TG98 08XBV9 054297 09F6B7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

SUMMARIES

			Description	08x1a3 colletotric	09p960 aspergillus	Ostabs monilinia f	09v7q8 pyrenopeziz	08x1p1 blumeria gr	006319 mycobacteri	O9kk87 mycobacteri	Q9xb09 mycobacteri	O69691 mycobacteri	059893 penicillium	053581 mycobacteri	006793 mycobacteri	Q9cdb3 mycobacteri	030349 raistonia s	Q8tyq4 methanopyru	086787 streptomyce
CHTYUMINOC			. OI	08X1A3	096360	OBTGB8	Q9Y7G8	Q8X1P1	5 006319	Q9KK87	Ø9XB09	069691	059893	5 053581	006793	5 Q9CDB3	030349	OSTYQ4	9 086787
	æ		ngth DB	224 3	254 3	201 3	203 3	236 3	231 16	220 2	143 2	207 16	234 3	336 16	174 16	336 16	559 2	455 17	420 16
	æ	Query	Match Le	58.0	27.0	23.0	21.8	20.4	17.9	16.1	13.2	11.5	10.5	10.3	9.8	9.5	9.5	9.0	6.8
			Score	579	270	229.5	217.5	203.5	179	160.5	132	114.5	105	103	98	95	91.5	06	88
		Result	NO.		7	m.	4	S	9	7	8	σ	10	11	12	13	14	15	16

																			-				÷Τ			4	
RESULT 1	QBXIA3 PRELIMINARY; PRT; 224 AA.	2002 (TrEMBLrel.	(TrEMBLrel. 20, Last	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	Cutinase.	COLLECOLLICIUM GLOBOSPOLICIDES (ANTHRECHOSE LUNGUS) (GLOMETELLA Cinquiata)	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;	Glomerella.	NOB1_10X1D=040/;	SECTIENCE FROM N.A.	Abu Bakar F.D. Cooper D.M., Zamrod Z., Mahadi N.M., Sullivan P.A.	"Cloning and characterization of the cutinase-encoding gene and cDNA	from the fungal phytopathogen, Glomerella cingulata.";	Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.	EMBL; AF444194; AAL38030.1;	Interpro; IPRUU06/5; Cutinase. Dfam: DD01083; Cutinase: 1	FIGURE TO COLOR TO CO	PROSITE; PS00155; CUTINASE_1; UNKNOWN_1.	CUTINASE_2; U	SEQUENCE 224 AA; 23477 MW; 6E40C7343168ABDE CRC64;	%; Score 579; DB 3; Length 224; %; Pred. No. 3.6e-40;	Matches IIU; Conservative 29; Mismatches 47; Indels 2; Gaps	7 NGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHIRNIWIQGVGGPYDA 64	36 NELETGSSSACPKVIXIFARASTEPGNMGISAGPIVADALERIYGANDVWVQGGPYLA 95	65 ALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKE 124	
RES O8X	A D	DI	DŢ	텀	E C	S C	8	ပ္ပ	8	5 6	R P	Z.	RT	RŢ	RL	H :	7 C	DR	DR	DR	SO	о ш	4	Οy	QQ	Qγ	

```
Cutinase.
                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                           Local
                                                                                                                                                                                                                                                                                                                         Q9Y7G8
Q9Y7G8;
                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                 RESULT
Q9Y7G8
RT RT DK SO
                                                                                                           δ
                                                                                                                                                                         g
                                                                                                                                                                                                                     g
                                                                                                                                                      å
                                                                                                                                                                                                  à
                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
                  125 QVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIEARGEA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 TNFLPRGTSQANIDEGKRLFALANQ---KCPNTPVVAGGYSQGAALIAAAVSELSGAVKE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 ESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALA 67
                                                                                                                                                                                             Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-21927027; PubMed-11929215;
Wang G.Y., Michailides T.J., Hammock B.D., Lee Y.M., Bostock R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 QVKGVALFG--YTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-RIBLS.

X MEDLINE-20389597; Pubmed-10930731;
A Toida J., Fukusawa M., Kobayashi G., Ito K., Sekiguchi J.;
A Toida J., Fukusawa M., Kobayashi G., Ito K., Sekiguchi J.;
T "Cloning and sequencing of the triacylglycerol lipase gene of Aspergillus oryzae and its expression in Escherichia cili.";
EMEM STRODIOL. Lett. 189:159-164(2000).
REMSP; PO0590; IFFA.
RSSP; PO0590; IFFA.
RSSP; PO0590; IFFA.
RSSP; PO01083; Cutinase.
PRINTS; PRO1083; Cutinase.
RRINTS; PRO1083; Cutinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUTI.
Monilinia fructicola.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Monilinia.
NCBL_TaxID=38448;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.0%; Score 270; DB 3; Length 25 Best Local Similarity 33.9%; Pred. No. 1.3e-14; Matches 60; Conservative 36; Mismatches 63; Indels
                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 21, C
(TrEMBLrel. 21, I
(TrEMBLrel. 21, I
                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                    Triacylglycerol lipase
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                 185 ARFLRDRI 192
                                                                      216 PRFLOARI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cutinase.
                                                                                                                             Q9P960
Q9P960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8TGB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
Q8TGB8
                                                                                                        RESULT 2
                          g
       á
                                                  ð
                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
128 QLPAATTAKIAAAVIFG---DPDNGSPVQGVPAAKTKIICHAGDNICQHGSMILMP-HLT 183
                                                                                                                                                                                                                                                                                                                                                                                                                         62 YDAALATNFL----PRGTS-QANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 ELSGAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCT-GTLIITPAHLS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 ALATNFLPRG-----TSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELS 119
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 GAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYTIE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 AATMAKISSLVIFG---DPNDGKPIANADPSKVWVCHPGHNICDGRDLVLVEHLTYSRD 189
                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                            24 GEIE-----ARACSTVTVIFARGTTETPTLGTVIGPQFLAALKSSFGGSVTMNGV--P 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davies K.A., Ashby A.M., Johnstone K.;
Davies K.A., Ashby A.M., Johnstone K.;
Cloning of a cutinase gene from Pyrenopeziza brassicae: cause of ilight leaf spot disease of brassicas, and sequence comparison with other known fungal cutinases.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ009953: CAB40372.1;
HSSP; P00590; 1XzJ.
                                                                                                                                                                                                                                                                            3 GAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 GVDTTSSSPNCAEMMVVFARGTSEPGNVGLFSGPTFFDALEVVMGAGAVSVQGV--EYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GLESGSANA-CPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDA
"Molecular Cloning, Characterization, and Expression of a Redox-Responsive Cutinase from Monilinia fructicola (Wint.) Honey."; Fungal Genet. Biol. 35:261-276(2002).

EMBL; AF305598; AAM.0822.1; -SEQUENCE 201 AA; 20227 MW; EEA098D9E15019AA CRC64;
                                                                                                                                                                                                                           27;
                                                                                                                                                                    DB 3; Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.8%; Score 217.5; DB 3; Length 203; 31.3%; Pred. No. 2.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Dermateaceae; Pyrenopeziza.
NCBI_TaxID=76659;
                                                                                                                                                                                     ,2e-11;
.es 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00129; CUTINASE.
PROSITE; PS00155; CUTINASE_1; 1.
SEQUENCE 203 AA; 20525 MW; 01FB0B0BC42F7C46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 AA
                                                                                                                                                              23.0%; Score 229.5;
33.7%; Pred. No. 2.2e
iive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.3%; Pred. No. 2.2e
:ive 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000675; Cutinase.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                        64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyrenopeziza brassicae.
                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ::| ||
184 YGMDATAAAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 YTIEARGEAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=JH26;
```

8

```
Mycobacterium avium.
                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                              P00590; 1CUZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9KK87
                                                                                                                                                                                                                                                                                                                                                                                                                           Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Horrsby R., Pevlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       | :: | ||| || : | |||:|:
169 PLVISRIAAVVLFGDPYIDK-----PVGQVSPSSVLEICHDGDIICTGSGGPDP-HLIYS 222
                                                                                                                                                                                                                                                                                                                                                                                              DAALATNFLPRGTSQANIDEGKRLFALANQ----KCPNTPVVAGGYSQGAALIAAAVSELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAVKEQVKGVALFG - - YTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTLIITPAHLSYT 177
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                 7 NGLESGSANACPDAILIFARGSTEPGNM--GITVGPALANGLESHI--RNIWIQGVGGPY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 23.1 Kba protein (Serine esterase, cutinase family).
RV3452 OR MT3559 OR MTCY13E12.05.
                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                    Blumeria
                                                                                                                                                                                                                                                                                                                                   20.4%; Score 203.5; DB 3; Length 236; 33.8%; Pred. No. 3.7e-09; iive 30; Mismatches 76; Indels 23
                                                                                                                                                      Blumeria graminis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
                                                                                                                                                                                                                      Zhang Z., Perfect E., Gurr S.J.;
"Cutinase gene isolation and functional analysis from Blum graminis during the barley/powdery mildew interactions.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF326784; AAL67672.1;
InterPro; IPR000675; Cutinase.
PROSITE; PS00155; Cutinase.
PROSITE; PS00155; CUTINASE_1;
SEQUENCE 236 AA; 24604 MW; 6528C4F26A4AFCEC CRC64;
                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 AA.
                                                                            AA.
                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98295987; PubMed-9634230;
                                                                                                 20,
20,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                            Conservative
            | ||| | ||:|
190 A-VEAATFAAARAKA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 IEARGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
ARGEAARFLRDRIRA 194
                                                                           PRELIMINARY;
                                                                                               01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=34373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                        Local Simple 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=H37RV
                                                                                                                                  Cutinase.
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                      Q8X1P1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              006319
                                                                         08X1P1
                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
006319
                                                      RESULT 5
                                                                 õ
                  g
                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
SQANIDEGKRLFALANQKCPNTPVVAGGYSQGAA---LIAAA----VSELSGAVKEQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GANDASDHIQQMASA---CRATRLVLGGYSQGAAVIDIVTAAPLPGLGFTQPLPPAADDH 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 VKGVALFGYTQNLQNRGG-----IPNYPRERTKVFCNVGDAVCT-GTLIITPAHLSYTI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 CPDAILIFARGSTEPGNMGITVGPALANGLESHI-RNIWIQGVGGPYDAALATNFLPRGT 75
                                                                                                                                                                                                                                                       STRAIN-CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole genome comparison of Mycobacterium tuberculosis clinical and
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-969445; TISSUE-BLOOD;
Carroll J.D., Wallace R.C., Keane J., Arbeit R.D.;
Tidentification of Mycobacterium avium DNA Sequences that is
Exported Proteins by Using phoA Gene Fusions.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF139058; AAF74988.1; -.
InterPro; IPR000675; Cutinase.
InterPro; IPR000379; Set_estrs_site.
Pfam; PF01083; Cutinase; 1.,
PROSITE; PS00155; CUTINASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 protein; Complete proteome.
231 AA; 23686 MW; 45943C6B23FFB480 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9KK87 PRELIMINARY; PRT; 220 AA. Q9KK87; Q1-COT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Serine esterase cutinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.9%; Score 179; DB 16; 32.5%; Pred. No. 3.8e-07; tive 24; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tuberculist; RV3452; --
InterPro; IPR000675; Cutinase.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF01083; Cutinase; I.
Hypothetical protein; Complete protec
SEQUENCE 231 AA; 23686 MW; 459430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 295390; CAB08718.1; ALT_INIT
EMBL; AE007160; AAK47898.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Conservative
                                                                                                                                                                     Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :||||: ||
GMTNQAARFVASRI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 EARGEAARFLRDRI 192
```

```
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                      NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MT3827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998
01-AUG-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bishai W.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          059893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
059893
        δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of variable regions in the genomes of tubercle bacilli using bacterial artificial chromosome arrays.";
Mol. Microbiol. 32:643-655(1999).
EMBL: Y18666; CAB44660.1; -.
HSSP; P00590; 1XZJ.
                                                                                                                                                                                                                       71 LPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELSGAVKEQVKGVA 130
                                                                                                                                                                                                                                              84 DYHNSANAGADDASAHVQDTVAACPNSRIVLGGYSQGSTVIDLATNAMPPSVADHVAAVA 143
                                                                                                                                                                                                                                                                                                      LF----GYTQNLQNRGGIPNYP---RERTKVFCNVGDAVCTGTLITTPAHLSYTIEA-- 180
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                         13 SANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALATNF 70
                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SANACPDAILIFARGSTEPGNMGITVGPALANGLESHI--RNIWIQGVGGPYDAALATNF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 SDGACPDVEVVFARGTGEPPGVG-GIGEDFIDALRSKIGEKSMGVYGVDYP----ATTD
                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gordon S.V., Brosch R., Billault A., Garnier T., Eiglmeier K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 LPRGTSQANI-DEGKRLFALANQKCPNTPVVAGGYSQGAALI----AAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 13.2%; Score 132; DB 2; Length 14 Local Similarity 36.6%; Pred. No. 0.0016; les 41; Conservative 19; Mismatches 36; Indels
                                                                                                      Indels
CUTINASE_2; UNKNOWN_1.
22394 MW; CBFAF9F47FF65D9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6CBA62B8174755E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                            DB 2;
                                                        ch 16.1%; Score 160.5; DB 2
1 Similarity 28.1%; Pred. No. 1.2e-05;
54; Conservative 35; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-BCG-PASTEUR;
MEDLINE-99255698; PubMed=10320585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01083; Cutinase.
NON_TER 143 143
SEQUENCE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 07, CTrEMBLrel. 20, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17, RVD2-RV1758 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium bovis BCG
                                                                                                                                                                                                                                                                                                                                                                                 181 RGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                       202 TAQAATFAANHL 213
                                                                           Local Similarity
PROSITE; PS00931;
SEQUENCE 220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (
01-MAR-2002 (
01-MAR-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVD2-RV1758
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               069691
069691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca]
Matches
                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09XB09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
069691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                          βp
                                                                                                                                                                               셤
                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC DRT REP BE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DA LA LA
```

```
Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 -------IAAAVSELSGAVKEQVKGVALFG--YTQNLQNRGGIP----NYPRE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 RNIWIQGVGGPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 KSLGVYAVNYPASNDFASSDFPKTVIDGIRDAGSHIQSMA-MSCPQTRQVLGGYSQGAAV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 AGYVTSAVVPPAVPVQAVPAPMAPEVANHVAAVTLFGAPSAQFLGQYGAPPIAIGPLYQP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Eatt D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Deloher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                       Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Fungi, Aścomycota, Pezizomycotina, Eurotiomycetes;
Eurotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
NCBI_TaxID=28575;
                                                                                                                                                                                                                                                                                                                                                                 Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Bardocck K., Bashman D., Brown D., Chillingworth T., Connor R., Davies R., Deviln K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Osborne J., Oshorne J., Moule S., Murphy L., Oliver S., Csborne J., Quall M.A., Rajandram M.A., Rogers J., Rutter S., Seeger K., Skelton S., Stalston J.E., Taylor K., Whitehead S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
   (Serine esterase, cutinase family)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.5%; Score 114.5; DB 16; Length 26.4%; Pred. No. 0.071; ive 22; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory strains.",
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO2213; CAA18046.1; ALT_INIT.
EMBL; AE007179; AAK48196.1;
                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 AA; 21225 MW; 967510FD7C49D7D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 RIKVFCNVGDAVCTGTLIITPAHLSYTIEAR-GEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Acetyl xylan esterase II (EC 3.1.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 AA
                                                                                                                                                                                                                                                                                                                                     MEDLINE=98295987; PubMed=9634230;
Putative cutinase precursor (Se RV3724 OR MT3827 OR MTV025.072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculist; Rv3724; -- InterPro; IPR000675; Cutinase. Pfam; PF01083; Cutinase; 1.
                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penicillium purpurogenum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
```

9

ស

ŝ

Gaps

```
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-9825987; PubMed-9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Cole S.T., Brosch R., Fallmeil J., Garnier T., Churcher C., Harris D.,
Cole S.T., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
"Deciphering the biology of Mycobacterium tuberculosis from the
Complete genome sequence.";
                                                                                                                                                                                                                                                                                                 ----- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 YDAALATNFLPRGTSQANIDEGKRLFALA----NQKCPNTPVVAGGYSQGAALIAAAVSE 117
                                                                                                                                                                                                                                                                                                                                                                                        131 HNPLTTDNQMSYNDSRA---EGTRAMVAAMTDMNNRCPLTSYVLIGFSQGAVIAGDVASD 187
                                                                                                                                                                                                                                                                         ACPDAILIFARGSTE------PGNMGITV-GPALANGLESHIRNIWIQCVGGP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 17.9 kba protein (Serine esterase, cutinase family).
RV1758 OR MTCY28.24 OR MT1805.
                                                                                                                                                                                              Length 336;
                                                                                                                                                                                                                                    Indels
                    laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022076; CAA17866.1; -.
EMBL; AE007184; AAK48275.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL/GenBank/DDBU databases.
EMBL; 295890; CAB09321.1; -.
                                                                                                                                     .l protein; Complete proteome.
336 AA; 35448 MW; F374D163449C6547 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              118 LS---GAVKEQ-VKGVALFGYTQNLQNRGG-IPNYPR------
                                                                                                                                                                                                                                  86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ERTKVFCNVGDAVCTG-TLIITPAHLSYTI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRPGGFGALDGRTNEICAQGDLICAAPAQAFSPANLPTTL 287
                                                                                                                                                                                          10.3%; Score 103; DB 16; 22.7%; Pred. No. 1.1; ive 24; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE007040; AAK46078.1; -. HSSP; P00590; 1CUU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CDC 1551 / OSHKOSH;
                                                                                                                                                                                                                                  Conservative
                                                                                                               Tuberculist; Rv3802c; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory strains.";
                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1773;
                                                                                               TIGR; MT3909;
                                                                                                                                     Hypothetical
SEQUENCE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-H37RV
                                                                                                                                                                                                                                  50;
                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               006793
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
006793
    SWRDBRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAINS-CDC 1551 / OSHKOSH;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                            ဌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 -- AYPGSTAEAINYPACGGQSSCGGASYSSSVAQGIAAVASAVNSFNSQCPSTKIVLVGY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 SQGGEIMDVALCGGGDPNQGYTNTAVQLSSSAVNMVKAAIFMGDPMFRAGLSYEVGTCAA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 GVGGPYDAALAINFIPRG-----TSQANIDEGKRIFALA----NQKCPNTPVVAGGY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 SQGAALIAAAVS-----YTQNLQNR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s:
                                                                                                                                                                                                                                                                                                                                                                                  2 LGA----IENGLESGSANACPDAILIF-ARGSTEPGNMGITVGPALANGLESHIRNIWIQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 GGIPNYP-----RERTKVFCNVGDA-VCTGTLIITPAHLSYTIEARGEAARFLRDRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 GGFDQRPAGFSCPSAAKIKSYCDASDPYCCNGSNAAT--HQGYGSFYGSQALAFVKSKL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STEAIN-#37RV;
MEDLINE-98295987; PubMed-9634230;
Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier K., Paskhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eiglmeier R., Barnam D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Erown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Stulton J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
              Gutierrez R., Cederlund E., Hjelmqvist L., Peirano A., Herrera F., Gobsh D., Duax W., Jernvall H., Eyzaguirre J.;
"Accetyl xylan esterase II from Penicillium purpurogenum is similar an esterase from Trichoderma reesel but lacks a cellulose binding
                                                                                                                                                                                                                                                                                                                                                                                                    13 LGAAAIPLEGVMEKRS---CP-AIHVFGARETT--ASPGYGSSSTVVNGVLS-----
                                                                                                                                                                                                                                                                                                                                                   :99
                                                                                                                                                                                                                                                                                                       10.5%; Score 105; DB 3; Length 234; 23.8%; Pred. No. 0.5; ative 30; Mismatches 86; Indels
                                                                                                                                                                                                                                                  28 234 AA; C033B3DA4E7BB6E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv3802c.
RV3802C OR MTV026.07C OR MT3909.
Mycobacterium tuberculosis.
                                                                                                                                                                                                            PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
MEDLINE-98165682; PubMed-9506837;
                                                                                                           FEBS Lett. 423:35-38(1998).
EMBL, AF015285; AAC39371.1; -
Interpro; IPR000675; Cutinase.
InterPro; IPR000734; Lipase.
Pfam; PF01083; Cutinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1773;
                                                                                                                                                                                                                                  Hydrolase.
                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete
                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          053581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
053581
                                                                                                                                                                                                                                                                                                                                                 Matches
8
                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
```

```
030349
                                                                                                       030349
     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
                                                                  14
                                                                  RESULT
                                                                            030349
      ò
                            셤
                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>a</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                        NGLESHI--RNIWIQGVGGPYDAALATNFLPRGTSQANI-DEGKRLFALANQKCPNTPVV 100
                                                                                                                                                                                                                63 LGGFSQGAAVMGFVTAAAIPDGAPLDAPRPMPPEVADHVAAVTLFGMPSVAFMHSIGAPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                       101 AGGYSQGAALI ---- AAAVSE-----LSGAVKEQVKGVALFGY--TQNLQNRGGIP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 GGPYDAALATNFLPRGTSQANID----EGKRLFAL----ANQKCPNTPVVAGGYSQGAAL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:: | | : | | | : | | | AGDITSDIGNGHGPVDDDLVLGVTLIADGRRQQGVGNDIGPNPPGEGAEVTLHEVPVLSG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 IAAAVSELS---GAVKEQ-VKGVALFGYTQNLQNRGGI--PNYPRE--------- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                               DALRSKIGEKSMGVYGVDYP----ATTDFP--TAMAGIYDAGTHVEQTA-ANCPQSKLV 62
                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium leprae.
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ACPDAILIFARGSTEPG-------NMGITVGPALANGLESHIRNIWIQGV
                                                                                                                                                                                                                                       ----NYPRERTKVFCNVGDAVCT--GTLIITPAHLSYTIEARGE-AARFLRDRI 192
                                                                                                                                                                                                                                                               123 IVIGPLYAEKTIQLCAPGDPVCSSGGN---WAAHNGYADDGMVEQAAVFAAGRL 173
                                                                                         Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86; Indels
                                                                                                                 Indels
TIGR; MT1805; -.
Tuberculist; Rv1758; -.
Interpro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 174 AA; 17868 MW; 36684DEB29AE73C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
SEQUENCE 336 AA; 35610 MW; 2D3B558AB526F633 CRC64;
                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                64;
                                                                                      9.8%; Score 98; DB 16;
llarity 29.9%; Pred. No. 1.3;
Conservative 22; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.5%; Score 95; DB 16;
22.5%; Pred. No. 5.2;
Live 19; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EBMBU; AS3917; CAC29607.1; -.
                                                                                                                                                                                                                                                                                                                               Ā
                                                                                                                                                                                                                                                                                                                              336
                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                       01-0CT-2001 (TrEMBLrel. 17, 01-0CT-2001 (TrEMBLrel. 18, Hypothetical protein ML0099, ML0099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001
                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                      Local
                                                                                                                                                                                                                                                                                                                            09CDB3
                                                                                                                Matches
                                                                                                                                                               11
                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                 Q9CDB3
   g
                                                                                                                                                                                       à
                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

```
Allen C., Gay J., Simon-Buela L.;
"A regulatory locus, pehSR, controls polygalacturonase production and other virulence functions in Ralstonia solanacearum.";
Mol. Plant Microbe Interact. 10:1054-1064(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAAVSELS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 GSADLAERTNALLPGHSAAMQEVRRSLLRLARSMAP--VVISGESGSGKERAARAIHALS 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GAVKEQVKGVALFGYTQNLQNRGGIPNYPRERTKVFCNVGDAVCTGTL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING
-RTKVFCNVGDAVCTG----TLIITPAHLSYTIEARGE 183
                                            241 LGMTMTGARPGGFGVLHSRTNEICAPGDLICAAPAEAFSVANLPATLNTLASGAGQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO1199; HTH_fis; 1.
PROSTIE: PSO0676; SIGMAS4_INTERACT_2; UNKNOWN_1.
PROSTIE: PS50045; SIGMAS4_INTERACT_4; 1.
ATP-binding; DNA-binding; Phosphorylation; Sensory transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 SGSANACPDAILIFARGSTEPGNMGITVG--PALANGLE-SHIRNIWIQGVG----
                                                                                                                                                                                                                                                                                                                                       Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60070 MW; 531BD5E392B558F9 CRC64;
                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                    Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.2%; Score 91.5; DF
26.4%; Pred. No. 19;
tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    455
                                                                                                                                                                    559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 IITP-AHLSYTIEARGEAARFLRD-RIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLDEVADLPLTMOVK - - LLRRLQDGRVR 268
                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98052122; PubMed=9390420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P41789; INTR.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR002197; HTH_Fis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF001171; AAC24599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 26.48
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation.
SEQUENCE 559 AA; 60070
                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00382; AAA; 1
SMART; SM00448; REC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                      Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
Q8TYQ4
ID Q8TYQ4
AC Q8TYQ4;
```

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                               Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
Methanopyrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 INFLPRGTSQ---ANIDEGKRLFALA------NQKCPNTPVVAGGYSQG-AALI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 PDA-ILIFARGST--EPGNMGITVGPALA-----NGLESHIRNIWIQGVGGPYDAALA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.0%; Score 90; DB 17; Length 455; Best Local Similarity 26.7%; Pred. No. 19; Matches 43; Conservative 20; Mismatches 58; Indels
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit.
GATA OR MK0238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 AAGLCDAALGSDTGGSIRNPASHCGVVGFKPTYGLVPROGL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 AAAV-----SELSGAVKEQVK--GVALFGYTQNLQNRGGI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE-21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2320;
                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
```

Search completed: January 2, 2003, 15:06:17 Job time : 32 secs

THIS PAGE BLANK (USPTO)

Bond A. I have the formation of the form